

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2004, 14:01:27 ; Search time 2154 Seconds
(without alignments)
12638.093 Million cell updates/sec

Title: US-09-996-128A-1

Perfect score: 1 atctctcagatccacgac.....tctatttaaaaccgga 6408

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: geneseq19808:.*
2: geneseq19908:.*
3: geneseq20008:.*
4: geneseq20018:.*
5: geneseq20028:.*
6: geneseq20038:.*
7: geneseq20048:.*
8: geneseq20058:.*
9: geneseq20068:.*
10: geneseq20078:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6408	100.0	6408	7	ABX10643 Vector, h
2	5636	88.0	6485	7	ABX10644 Vector, h
3	2878.4	44.9	5385	9	ADDD35598 Bistron
4	2878.4	44.9	7086	9	ADDD35600 Tricistron
5	2878.4	44.9	7334	9	ADDD35601 Tetracist
6	2378.8	37.1	5089	7	ABZ59287 Plasmid p
7	2378.8	37.1	5089	7	ABZ59290 Plasmid p
8	2378.8	37.1	5488	7	ABZ59291 Plasmid p
9	2378.8	37.1	5488	7	ABZ59288 Plasmid p
10	2378.8	37.1	5500	7	ABZ59289 Plasmid p
11	2378.8	37.1	5500	7	ABZ59286 Plasmid p
12	2027.6	31.6	10466	9	ADDE06467 Vector pg
13	2027.6	31.6	10466	9	ADDE06466 Vector pg
14	2027.2	31.6	10447	9	ADDE06463 Vector pg
15	2027.2	31.6	10447	9	ADDE06462 Vector pg
16	2020.8	31.5	9918	6	AA519260 DNA vacci
17	2008.6	31.3	5108	4	AAAC86259 Plasmid G
18	2008.6	31.3	5108	4	AAAC86258 Plasmid G
19	2008.6	31.3	5108	4	ABK53269 Growth ho
20	2008.6	31.3	5111	4	ABK53270 Growth ho
21	2008.6	31.3	5111	4	AAAC86262 CMV IE pr
22	2008.6	31.3	5111	6	ABK53273 Growth ho
23	2008.6	31.3	5185	4	AAAC86254 pGHRH-4 c

24	2008.6	31.3	5185	6	ABK53265 Growth ho
25	2008.6	31.3	5188	4	AAAC86266 Plasmid G
26	2008.6	31.3	5188	6	ABK53277 Growth ho
27	2008.6	31.3	5254	4	AAAC86267 Plasmid p
28	2008.6	31.3	5254	6	ABK53601 Growth ho
29	2005.8	31.3	10447	9	ADDE06464 Vector pg
30	1993.8	31.1	10446	9	ADDE06465 Vector pg
31	1665.2	30.7	5899	7	ABSS5905 DNA plasm
32	1555.6	30.5	7528	4	AAAF30316 Bistron
33	1542.2	30.3	5843	7	AAAV00676 DNA plasm
34	1492.2	30.3	5845	7	ABSS5904 DNA plasm
35	1325.4	30.0	5898	2	AAV00677 DNA plasm
36	1292.4	29.5	2041	4	AA560958 Human can
37	1192.4	29.5	1894	2	AAO06552 Clone BBT
38	1890.8	29.5	1894	2	AAAT01009 Human tyr
39	1890.8	29.5	1894	2	AAAT75678 Human SK2
40	1886.6	29.4	1964	7	ABO83843 Human tyr
41	1886.6	29.4	1964	9	ADCO9569 Tyrosinas
42	1886.6	29.4	2384	2	AAAT33316 Tyrosinas
43	1886.6	29.4	2384	2	ABO76197 Human tum
44	1885	29.4	1906	2	AAQ6548 Human tyr
45	1885	29.4	1910	2	AAAT35901 Tyrosinas

ALIGNMENTS

RESULT 1	ABX10643
ID	ABX10643 standard; DNA; 6408 BP.
XX	AC
XX	ABX10643;
XX	DT
XX	22-APR-2003 (first entry)
DE	Vector, htyr-pING, containing human tyrosinase gene.
XX	KW
XX	Human; gene; de; melanoma; xenogeneic differentiation antigen; DA; PING;
XX	KW
XX	tyrosinase; canine; gene therapy; dog; cytostatic.
XX	OS
XX	Homo sapiens.
PN	US2002150589-A1.
XX	PD
XX	17-OCT-2002.
XX	XX
PF	27-NOV-2001; 2001US-00996128.
XX	XX
PR	10-DEC-1996; 96US-0032535P.
PR	18-FEB-1997; 97US-0036419P.
PR	10-DEC-1997; 97WO-US022669.
PR	21-MAY-1999; 99US-00308697.
PR	26-JAN-2000; 2000US-0180651P.
PR	28-JUL-2000; 2000US-00627694.
XX	XX
PA	(HOUG/) HOUGHTON A N.
PA	(BERG/) BERGMAN P J.
PA	(WOLC/) WOLCHOK J D.
PI	Houghton AN, Bergman PJ, Wolchok JD;
XX	XX
DR	WPI; 2003-182484/18.
PT	PT
PT	Treating melanoma in a mammalian subject comprises administering to the
PT	subject an immunological amount of a xenogeneic differentiation antigen
PT	of the same type as a differentiation antigen expressed by melanoma cells
PT	of the subject.
PS	Claim 26; Page 5-8; 15pp; English.
XX	XX
CC	The invention discloses a method for treating melanoma in a mammalian
CC	subject which comprises administering to the subject an immunological
CC	amount of a xenogeneic differentiation antigen (DA) of the same type as a

CC DA expressed by melanoma cells of the subject. Also disclosed are pING
CC vectors containing a sequence encoding the human or mouse tyrosinase
CC genes. The methods and xenogeneic DA are useful for treating canine
CC malignant melanoma (gene therapy) in dog suffering from the disease by
CC administering an immunological amount of the xenogeneic DA and for other
CC mammals. The sequence presented is the vector, hcyr-pING, containing the
CC human tyrosinase gene
XX

SQ Sequence 6408 BP; 1621 A; 1583 C; 1509 G; 1695 T; 0 U; 0 Other;

Query Match 100.0%; Score 6408; DB 7; Length 6408;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATTCTGAGATATCTCAGACAGTGGCGGCGCTCGAATCTAGAGGGCCGTTTAAACCG 60
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Db 1 ATTCTGAGATATCTCAGACAGTGGCGGCGCTCGAATCTAGAGGGCCGTTTAAACCG 60

QY 61 CTGATCAGCTCGACTGTGCTTCTAGTTGCCAGCCATCTGTTTCCCTCCCGCT 120
   |||||
Db 61 CTGATCAGCTCGACTGTGCTTCTAGTTGCCAGCCATCTGTTTCCCTCCCGCT 120

QY 121 GCGTTCCTTGAACCTTGAGAGAGTGCACATCCCACTGCTCTTCTTAATAAATAGAGAAAT 180
   |||||
Db 121 GCGTTCCTTGAACCTTGAGAGAGTGCACATCCCACTGCTCTTCTTAATAAATAGAGAAAT 180

QY 181 TGCATCGCATTTGTCTGAGTAGTGTCAATCTATTCTGGGGGGTGGGGTGGGCGAGAG 240
   |||||
Db 181 TGCATCGCATTTGTCTGAGTAGTGTCAATCTATTCTGGGGGGTGGGGTGGGCGAGAG 240

QY 241 CAAGGGGGAGATTGGGAGAACATATAGCAGCATGTGGGGATGCAAGGGGGGGGGGCG 300
   |||||
Db 241 CAAGGGGGAGATTGGGAGAACATATAGCAGCATGTGGGGATGCAAGGGGGGGGGGCG 300

QY 301 CTGAGGCTGCGCTCTGTAAGAGAGTGTGCTGACTACATCAAGGCTGGAATCGCCCATC 360
   |||||
Db 301 CTGAGGCTGCGCTCTGTAAGAGAGTGTGCTGACTACATCAAGGCTGGAATCGCCCATC 360

QY 361 ATCCAGCAGAAAGTAGAGAGAGCCACGTTGATGAGAGCTTGTGTGAGGTGAGCAGTT 420
   |||||
Db 361 ATCCAGCAGAAAGTAGAGAGAGCCACGTTGATGAGAGCTTGTGTGAGGTGAGCAGTT 420

QY 421 GGTGATTTGAACCTTTTGTGCGACGAAACGCTGCGTGTGCGGAAAGATGCGTAT 480
   |||||
Db 421 GGTGATTTGAACCTTTTGTGCGACGAAACGCTGCGTGTGCGGAAAGATGCGTAT 480

QY 481 CTGATCCTTGAACCTCAGCAAAAGTTGATTTATTCACAAAGCCGCTCCCTCAAGTC 540
   |||||
Db 481 CTGATCCTTGAACCTCAGCAAAAGTTGATTTATTCACAAAGCCGCTCCCTCAAGTC 540

QY 541 AGCGTAATGCTCTGCCAGTGTACCAACCAATTAACAATCTGATTTGAAAACTCATCG 600
   |||||
Db 541 AGCGTAATGCTCTGCCAGTGTACCAACCAATTAACAATCTGATTTGAAAACTCATCG 600

QY 601 AGCATCAATAGAACTGCAATTTATTCATATCAGAGATTATCAATATTTTGGAAA 660
   |||||
Db 601 AGCATCAATAGAACTGCAATTTATTCATATCAGAGATTATCAATATTTTGGAAA 660

QY 661 AGCGCTTCTGTATAGAGAGAAACTCACCAGGAGGAGTTCCATAGAGGCAAGATCC 720
   |||||
Db 661 AGCGCTTCTGTATAGAGAGAAACTCACCAGGAGGAGTTCCATAGAGGCAAGATCC 720

QY 721 TGGTATCGGTCTGCGATTCCGACTGTCACCAATCAATCAACTATTAATTTCCCTCG 780
   |||||
Db 721 TGGTATCGGTCTGCGATTCCGACTGTCACCAATCAATCAACTATTAATTTCCCTCG 780

QY 781 TCAAAAATTAAGTTATCAAGTAGAATAATCAACATGATGAGACTGAATCCGGGAGAAT 840
   |||||
Db 781 TCAAAAATTAAGTTATCAAGTAGAATAATCAACATGATGAGACTGAATCCGGGAGAAT 840

QY 841 GGCAGAAAGCTTATGCAATTTCTTCCAGACTTTGTTCACAGGCCAGCATTAACGTCGTCA 900
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Db 841 GGCAGAAAGCTTATGCAATTTCTTCCAGACTTTGTTCACAGGCCAGCATTAACGTCGTCA 900
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QY 901 TCAAAATCACTGCAATCAACCAACCGTATTCATTCGTGATTTGGCGCTGACGAGCA 960
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Db 901 TCAAAATCACTGCAATCAACCAACCGTATTCATTCGTGATTTGGCGCTGACGAGCA 960

QY 961 AATAGCGATTCGCTGTTAAAGACATTTACAAACAGAAATGAATGCAACCGGCGAG 1020
   |||||
Db 961 AATAGCGATTCGCTGTTAAAGACATTTACAAACAGAAATGAATGCAACCGGCGAG 1020

QY 1021 AACCTGCAAGCGCATCAACATATTTTACCTGAAATCGAGATTTCTTAATACCTG 1080
   |||||
Db 1021 AACCTGCAAGCGCATCAACATATTTTACCTGAAATCGAGATTTCTTAATACCTG 1080

QY 1081 AATGCTGTTTTCCCGGGATTCGACGTGTGATGAACATGATCATCAGAGTAGAGATA 1140
   |||||
Db 1081 AATGCTGTTTTCCCGGGATTCGACGTGTGATGAACATGATCATCAGAGTAGAGATA 1140

QY 1141 AAATGCTGATGAGTGGAGAGAGCATTAATTCGTGACGCAATTAATGTCACATCTCA 1200
   |||||
Db 1141 AAATGCTGATGAGTGGAGAGAGCATTAATTCGTGACGCAATTAATGTCACATCTCA 1200

QY 1201 TCTGTAACTCAATGAGCAACGCTACCTTGGCATGTTTCAGAAACAATCTGGCGCATG 1260
   |||||
Db 1201 TCTGTAACTCAATGAGCAACGCTACCTTGGCATGTTTCAGAAACAATCTGGCGCATG 1260

QY 1261 GCGTTCCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
   |||||
Db 1261 GCGTTCCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320

QY 1321 TTATACCAATTAATCAACATCATGATGATGATGATGATGATGATGATGATGATGATG 1380
   |||||
Db 1321 TTATACCAATTAATCAACATCATGATGATGATGATGATGATGATGATGATGATGATG 1380

QY 1381 TCCCGTGAATATGAGTCAATACCCCTGATTAATGATTAATGATTAATGATTAATGAT 1440
   |||||
Db 1381 TCCCGTGAATATGAGTCAATACCCCTGATTAATGATTAATGATTAATGATTAATGAT 1440

QY 1441 ATGTTATCATGATGATTAATTTTATCTGATGATTAATCATCAGAGATTTTGAACACA 1500
   |||||
Db 1441 ATGTTATCATGATGATTAATTTTATCTGATGATTAATCATCAGAGATTTTGAACACA 1500

QY 1501 AGGTGCTTTCCCGCCCCCGCGACGAGTTTCTTTTCCCAACCCCAACCCCAAG 1560
   |||||
Db 1501 AGGTGCTTTCCCGCCCCCGCGACGAGTTTCTTTTCCCAACCCCAACCCCAAG 1560

QY 1561 TTGCGGTGAAGGCGCAGGCTGCGACCAACGTCGGGGGGGAGAGCCGTCATAGCTTC 1620
   |||||
Db 1561 TTGCGGTGAAGGCGCAGGCTGCGACCAACGTCGGGGGGGAGAGCCGTCATAGCTTC 1620

QY 1621 AGGTATCATATATATCTTTAGATTGATTTAAACCTTCAATTTTAAATTAAGATCTTA 1680
   |||||
Db 1621 AGGTATCATATATATCTTTAGATTGATTTAAACCTTCAATTTTAAATTAAGATCTTA 1680

QY 1681 GGTGAAGATCTTTTGTATATCTCATGACCAAAATCCTTAAACGTGAGTTTCTGTCA 1740
   |||||
Db 1681 GGTGAAGATCTTTTGTATATCTCATGACCAAAATCCTTAAACGTGAGTTTCTGTCA 1740

QY 1741 CTGAGCGTGAACCCCGTGAAGAAAGATCAAAAGATCTTGAAGATCTTTTCTGCG 1800
   |||||
Db 1741 CTGAGCGTGAACCCCGTGAAGAAAGATCAAAAGATCTTGAAGATCTTTTCTGCG 1800

QY 1801 CGTATCTGCTCTTGAACCAAAAAACAACCGCTACCAAGCGTGTGTTTGTGCGGA 1860
   |||||
Db 1801 CGTATCTGCTCTTGAACCAAAAAACAACCGCTACCAAGCGTGTGTTTGTGCGGA 1860

QY 1861 TCAAGAGCTTACCAACTCTTTTCCAGAGTAACTGGCTTCAGAGAGCGCAATACAAA 1920
   |||||
Db 1861 TCAAGAGCTTACCAACTCTTTTCCAGAGTAACTGGCTTCAGAGAGCGCAATACAAA 1920

QY 1921 TACTGTTCTTGAAGTGAAGGATGAGTGAAGGACCACTTCAAGAACTGTGACACGCGC 1980
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Db 1921 TACTGTTCTTGAAGTGAAGGATGAGTGAAGGACCACTTCAAGAACTGTGACACGCGC 1980
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Db 4141 GGGTATGTGTCTGAAAAATGAGCTCGAGATTGGGCTTCGACCGCTGACGAGATGGAAGA 4200
Qy 4201 CTTAAGCAGCGGAGAGAAATGACGAGAGCTGAGTTGTGATTTCTGATAAGATCA 4260
Db 4201 CTTAAGCAGCGGAGAGAAATGACGAGAGCTGAGTTGTGATTTCTGATAAGATCA 4260
Qy 4261 GAGGTAACTCCCGTTGGGCTGTGTTAACGGTGGAGGGAGGTGAGTCTGAGAGATATC 4320
Db 4261 GAGGTAACTCCCGTTGGGCTGTGTTAACGGTGGAGGGAGGTGAGTCTGAGAGATATC 4320
Qy 4321 GTTGTGCGCGCGCGCGCACACAGATATATAGCTGAGATGACTAACAAGCTGTTCTTCC 4380
Db 4321 GTTGTGCGCGCGCGCGCACACAGATATATAGCTGAGATGACTAACAAGCTGTTCTTCC 4380
Qy 4381 ATGGGCTTTTCTGACAGTCAACCGTCAAGGCTTAAATACAGCTCATATAGAGAGACCAA 4440
Db 4381 ATGGGCTTTTCTGACAGTCAACCGTCAAGGCTTAAATACAGCTCATATAGAGAGACCAA 4440
Qy 4441 GCTGGCTAAGGCTTAAACCTTAAGCTTGTATCCGAGCTCGAGTCCATGTCAGTGTGT 4500
Db 4441 GCTGGCTAAGGCTTAAACCTTAAGCTTGTATCCGAGCTCGAGTCCATGTCAGTGTGT 4500
Qy 4501 GGAATTCGGGGAAGAAATGCTCTGCGCTGTTTGTATCTGCTGCTGAGAGTTTCCAGACC 4560
Db 4501 GGAATTCGGGGAAGAAATGCTCTGCGCTGTTTGTATCTGCTGAGAGTTTCCAGACC 4560
Qy 4561 TCCGCTGGCCATTTCCCTAAGAGCTGTCTCTCTAAGAACCTGATGAGAGAAATGC 4620
Db 4561 TCCGCTGGCCATTTCCCTAAGAGCTGTCTCTCTAAGAACCTGATGAGAGAAATGC 4620
Qy 4621 TGTCCACCGTGAAGCGGGGACAGAGATCCCTGTGGCAGGCTTTCAAGCAGAGTTCTGT 4680
Db 4621 TGTCCACCGTGAAGCGGGGACAGAGATCCCTGTGGCAGGCTTTCAAGCAGAGTTCTGT 4680
Qy 4681 CAGAAATCTCTTCTGTCCAAATGACCACTTGGGCTCAATTCCTTCAAGGGGTGAT 4740
Db 4681 CAGAAATCTCTTCTGTCCAAATGACCACTTGGGCTCAATTCCTTCAAGGGGTGAT 4740
Qy 4741 GACCGGAGTGTGGGCTTCCGCTTTTATATATGAGACCTGCGAGTCTCTGGCAATTC 4800
Db 4741 GACCGGAGTGTGGGCTTCCGCTTTTATATATGAGACCTGCGAGTCTCTGGCAATTC 4800
Qy 4801 ATGGGATTTCAACTGTGAAACTGCAAGTTTGGGCTTTGGGGAACCAACTGACAGAGAGA 4860
Db 4801 ATGGGATTTCAACTGTGAAACTGCAAGTTTGGGCTTTGGGGAACCAACTGACAGAGAGA 4860
Qy 4861 CGACTCTTGTGTGAGAAACAATCTTGATTTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 4920
Db 4861 CGACTCTTGTGTGAGAAACAATCTTGATTTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 4920
Qy 4921 GCTACTCTCACTTTAGCAAAAGCATACATCAGCTCAGACTATGTATCCCATAGGAGCC 4980
Db 4921 GCTACTCTCACTTTAGCAAAAGCATACATCAGCTCAGACTATGTATCCCATAGGAGCC 4980
Qy 4981 TATGGCCAAATGAAAAATGATCAACCAATGTTTAAAGCATCAATATTTATGACTTC 5040
Db 4981 TATGGCCAAATGAAAAATGATCAACCAATGTTTAAAGCATCAATATTTATGACTTC 5040
Qy 5041 TTTGTCTGTGATGCTTATATATGTGTCAATGATGCACTGTGGGGATATGAAATCTGG 5100
Db 5041 TTTGTCTGTGATGCTTATATATGTGTCAATGATGCACTGTGGGGATATGAAATCTGG 5100
Qy 5101 AGAGACATATATTTGGCCATGAAAGCAGCTTTCTGCTTGGCATATGACTTTCTTG 5160
Db 5101 AGAGACATATATTTGGCCATGAAAGCAGCTTTCTGCTTGGCATATGACTTTCTTG 5160
Qy 5161 TTGGGCTGGGAAACAAGAAATCCAGAGCTGACAGAGATGAAACCTTCACTATTCATAT 5220
Db 5161 TTGGGCTGGGAAACAAGAAATCCAGAGCTGACAGAGATGAAACCTTCACTATTCATAT 5220
Qy 5221 TTGGGATCTGGGGATGACAGAAAGTGTGACATTTTGCACAGATGATATGGAGGTGAG 5280
Db 5221 TTGGGATCTGGGGATGACAGAAAGTGTGACATTTTGCACAGATGATATGGAGGTGAG 5280
Qy 5281 CACCCCAAAATCTTAACCTTACTCAGCCGAGATCATTTCTCTCTTGGAGATTTGC 5340
Db 5281 CACCCCAAAATCTTAACCTTACTCAGCCGAGATCATTTCTCTCTTGGAGATTTGC 5340
Qy 5341 TGTAGCCGATTTGGAGAGATCAACAGCCATCAGTCTTTATGCAATGAAACGCCAGGGA 5400
Db 5341 TGTAGCCGATTTGGAGAGATCAACAGCCATCAGTCTTTATGCAATGAAACGCCAGGGA 5400
Qy 5401 CCTTTAGCGGCTAATCTGGAACCAATGCAATCCAGAACCCAGGCTCCCTCTTCA 5460
Db 5401 CCTTTAGCGGCTAATCTGGAACCAATGCAATCCAGAACCCAGGCTCCCTCTTCA 5460
Qy 5461 GCTGATGTGAATTTTCTGAGTTTGAACCAATATGAAATCTGTTCATGATTAAGCT 5520
Db 5461 GCTGATGTGAATTTTCTGAGTTTGAACCAATATGAAATCTGTTCATGATTAAGCT 5520
Qy 5521 GCCAATTTCACTTTGAAATACATGGAAGATTTGCTATGTCATTTCTGGATAGCG 5580
Db 5521 GCCAATTTCACTTTGAAATACATGGAAGATTTGCTATGTCATTTCTGGATAGCG 5580
Qy 5581 GATGCTCTCAAGCAGATGACAAATGCTTGCATCATCTATATGAAATGAAACATATGCC 5640
Db 5581 GATGCTCTCAAGCAGATGACAAATGCTTGCATCATCTATATGAAATGAAACATATGCC 5640
Qy 5641 CAGGTACAGGATCTGCAACGATCCTATCTTCTTCAAGAAATTTATCAAGAGCAAT 5700
Db 5641 CAGGTACAGGATCTGCAACGATCCTATCTTCTTCAAGAAATTTATCAAGAGCAAT 5700
Qy 5701 ATTTTGAAGATGAGTCTCGAAGAGCAGCTCTCTTCAAGAAATTTATCAAGAGCAAT 5760
Db 5701 ATTTTGAAGATGAGTCTCGAAGAGCAGCTCTCTTCAAGAAATTTATCAAGAGCAAT 5760
Qy 5761 GCACCATTTGACATACCGGGATCTCATGAGTTCTTTATACCATGTATACAGAAAT 5820
Db 5761 GCACCATTTGACATACCGGGATCTCATGAGTTCTTTATACCATGTATACAGAAAT 5820
Qy 5821 GGTATTTCTTTATTTCAATCAAAAGATCTGGCTATGACTATATGATCTAACAATTA 5880
Db 5821 GGTATTTCTTTATTTCAATCAAAAGATCTGGCTATGACTATATGATCTAACAATTA 5880
Qy 5881 GACCCAGACTCTTTTCAAGATCAATTAAGTCTTATTTGAAACAGAGAGTGGATCTGG 5940
Db 5881 GACCCAGACTCTTTTCAAGATCAATTAAGTCTTATTTGAAACAGAGAGTGGATCTGG 5940
Qy 5941 TCAATGCTCTTGGGCGGAGATGTGAGGGGCGGTCTGACGCTGCTGGCAGGGCTT 6000
Db 5941 TCAATGCTCTTGGGCGGAGATGTGAGGGGCGGTCTGACGCTGCTGGCAGGGCTT 6000
Qy 6001 GTGAGCTGTGTGTGTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6060
Db 6001 GTGAGCTGTGTGTGTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6060
Qy 6061 ATGGAAGAAAGAGATTAACAAGCTTGTATCAGAGCAATTTATAAAGCTTATAGCAAT 6120
Db 6061 ATGGAAGAAAGAGATTAACAAGCTTGTATCAGAGCAATTTATAAAGCTTATAGCAAT 6120
Qy 6121 GAGTAGGGCCAAAAGCCTGACCTCACTCACTCAAGTAATGTGCAGGTTCCAGAGA 6180
Db 6121 GAGTAGGGCCAAAAGCCTGACCTCACTCACTCAAGTAATGTGCAGGTTCCAGAGA 6180
Qy 6181 ATATGTCTGTATTTTTCTGTAAAGACCAATTTGCAAAATTTGATCAATCAAGTGT 6240
Db 6181 ATATGTCTGTATTTTTCTGTAAAGACCAATTTGCAAAATTTGATCAATCAAGTGT 6240
Qy 6241 AGCTTCTTCAACTCAGGTATGAAACACACTGTCTTGTCTGCTGTTTCACTCAGCCC 6300
Db 6241 AGCTTCTTCAACTCAGGTATGAAACACACTGTCTTGTCTGCTGTTTCACTCAGCCC 6300
Qy 6301 TTTTAACTTTTCCCTAAGCCCATATGTCTAAGAAAGAGTCTATTTGTGATATGAGA 6360
Db 6301 TTTTAACTTTTCCCTAAGCCCATATGTCTAAGAAAGAGTCTATTTGTGATATGAGA 6360
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QY 6361 ACTGTTATTTGATGATTAAGTCTCTATTTAAAAACCGGA 6408
DB 6361 ACTGTTATTTGATGATTAAGTCTCTATTTAAAAACCGGA 6408

RESULT 2
ID ABX10644 standard; DNA, 6485 BP.
XX ABX10644;
AC ABX10644;
XX
XX 22-APR-2003 (first entry)
XX
XX Vector, htyr-pING, containing mouse tyrosinase gene.
XX
XX Mouse; gene; ds; melanoma; xenogeneic differentiation antigen; DA; pING;
XX tyrosinase; canine; gene therapy; dog; cytosolic.
XX
XX Mus sp.
XX US2002150589-A1.
XX
XX 17-OCT-2002.
XX
XX 27-NOV-2001; 2001US-00996128.
XX
XX 10-DEC-1996; 96US-0032535P.
XX 18-FEB-1997; 97US-0036419P.
XX 10-DEC-1997; 97MO-US022659.
XX 21-MAY-1999; 99US-00308697.
XX 26-JAN-2000; 2000US-0180651P.
XX 28-JUL-2000; 2000US-00627694.
XX
XX (HOU/) HOUGHTON A N.
XX (BERG/) BERGMAN P J.
XX (WOLC/) WOLCHOK J D.
XX
XX Houghton AN, Bergman PJ, Wolchok JD;
XX
XX WPI; 2003-182484/18.
XX
XX Treating melanoma in a mammalian subject comprises administering to the
XX subject an immunological amount of a xenogeneic differentiation antigen
XX of the same type as a differentiation antigen expressed by melanoma cells
XX of the subject.
XX
XX Claim 27; Page 8-11; 15pp; English.
XX
XX The invention discloses a method for treating melanoma in a mammalian
XX subject which comprises administering to the subject an immunological
XX amount of a xenogeneic differentiation antigen (DA) of the same type as a
XX DA expressed by melanoma cells of the subject. Also disclosed are pING
XX vectors containing a sequence encoding the human or mouse tyrosinase
XX genes. The methods and xenogeneic DA are useful for treating canine
XX malignant melanoma (gene therapy) in dog suffering from the disease by
XX administering an immunological amount of the xenogeneic DA and for other
XX mammals. The sequence presented is the vector, htyr-pING, containing the
XX mouse tyrosinase gene
XX
XX Sequence 6485 BP; 1658 A; 1570 C; 1504 G; 1753 T; 0 U; 0 Other;
XX
XX Query Match 88.0%; Score 5636; DB 7; Length 6485;
XX Best Local Similarity 94.8%; Pred. No. 0;
XX Matches 5884; Conservative 0; Mismatches 270; Indels 56; Gaps 3;

QY 1 ATTCTGAGATATCATCAGACAGTGGCGGCTGAGTCTAGAGGCGCGTTTAAACCG 60
DB 1 ATTCTGAGATATCATCAGACAGTGGCGGCTGAGTCTAGAGGCGCGTTTAAACCG 60

QY 61 CTGATCAGCCTCGACTGCTGCTTCTAGTTGCGACCATCTGTTGTTGCCCTCCCGT 120
DB 61 CTGATCAGCCTCGACTGCTGCTTCTAGTTGCGACCATCTGTTGTTGCCCTCCCGT 120

QY 121 GCCTTCCTGACCCCTGGAAAGTGGCCATCCCACTGTCCTTCTAATAAATGAGGAAT 180
DB 121 GCCTTCCTGACCCCTGGAAAGTGGCCATCCCACTGTCCTTCTAATAAATGAGGAAT 180

QY 181 TGCATCGCATTTGCTGAGTAGTGTCTATTTCTGCGGCGGTGGGCGAGACAG 240
DB 181 TGCATCGCATTTGCTGAGTAGTGTCTATTTCTGCGGCGGTGGGCGAGACAG 240

QY 241 CAAGGCGGAGATTGGGAAAGACATAGCAGCATGCTGGGAGATGACGGGCGGCGG 300
DB 241 CAAGGCGGAGATTGGGAAAGACATAGCAGCATGCTGGGAGATGACGGGCGGCGG 300

QY 301 CTGAGGTCGCTCGTGAAGAAAGTGTGCTGCTATACAGGCGCTGAATCGCCCATC 360
DB 301 CTGAGGTCGCTCGTGAAGAAAGTGTGCTGCTATACAGGCGCTGAATCGCCCATC 360

QY 361 ATCCAGCCAGAAAGTAGAGGAGCAGGTTGATGAGAGCTTTGTTAGGTGACAGTT 420
DB 361 ATCCAGCCAGAAAGTAGAGGAGCAGGTTGATGAGAGCTTTGTTAGGTGACAGTT 420

QY 421 GGTGATTTTGAACCTTTTGTTCGACGGAACGCTGCTGCTGGGAAAGATGCTGAT 480
DB 421 GGTGATTTTGAACCTTTTGTTCGACGGAACGCTGCTGCTGGGAAAGATGCTGAT 480

QY 481 CTGATCCTTCATCTGACGAAAGTGTGATTTATTCACAAAGCGCGCTCCGTCAGTC 540
DB 481 CTGATCCTTCATCTGACGAAAGTGTGATTTATTCACAAAGCGCGCTCCGTCAGTC 540

QY 541 AGCGTAATGCTGCGCAGTGTTCACACCAATTAACCAATTTGATTAAGAAATCTACG 600
DB 541 AGCGTAATGCTGCGCAGTGTTCACACCAATTAACCAATTTGATTAAGAAATCTACG 600

QY 601 AGCATCAATGAAATCTGCAATTTATTCATATCATATGATTAATCAATATTTTGA 660
DB 601 AGCATCAATGAAATCTGCAATTTATTCATATGATTAATCAATATTTTGA 660

QY 661 AGCGTTTCTGTAATGAGGAGAAATCTACCGAGCAGTTCCATAGATGCAATATCC 720
DB 661 AGCGTTTCTGTAATGAGGAGAAATCTACCGAGCAGTTCCATAGATGCAATATCC 720

QY 721 TGGTATCGGTCGAGTCCGATTCGATTCGACATCAATCAATCAATTTTCCCTCG 780
DB 721 TGGTATCGGTCGAGTTCGATTCGATTCGACATCAATCAATCAATTTTCCCTCG 780

QY 781 TCAAAATTAAGGTTATCAAGTGAATCAACCATGAGTGAAT 840
DB 781 TCAAAATTAAGGTTATCAAGTGAATCAACCATGAGTGAAT 840

QY 841 GGCAAAAGCTTATGCAATTTCTTCGAGCTTGTCAACAGGCGCATTAAGCTGTCA 900
DB 841 GGCAAAAGCTTATGCAATTTCTTCGAGCTTGTCAACAGGCGCATTAAGCTGTCA 900

QY 901 TCAAAATCACTGCAATCAACCAAGCTTATTCATGATTTGGCGCTGAGGAGACGA 960
DB 901 TCAAAATCACTGCAATCAACCAAGCTTATTCATGATTTGGCGCTGAGGAGACGA 960

QY 961 AATACCGATCGCTGTTTAAAGGACATTAACAAGAGATGCAACCGCGCAGG 1020
DB 961 AATACCGATCGCTGTTTAAAGGACATTAACAAGAGATGCAACCGCGCAGG 1020

QY 1021 AACATGCGAGCGCATCAACATATTTTCACTGATCAAGATATTTCTTAATACCTGG 1080
DB 1021 AACATGCGAGCGCATCAACATATTTTCACTGATCAAGATATTTCTTAATACCTGG 1080

QY 1081 AATGCTGTTTCCCGGAGATCGAGTGTGATGATTAACATGATCAACAGAGTACGGA 1140
DB 1081 AATGCTGTTTCCCGGAGATCGAGTGTGATGATTAACATGATCAACAGAGTACGGA 1140

QY 1141 AAATGCTTATGATGATGAGGAGGATTAATTCGTCAGCGCATTTAGTGTACCATCTCA 1200
DB 1141 AAATGCTTATGATGATGAGGAGGATTAATTCGTCAGCGCATTTAGTGTACCATCTCA 1200

QY 1201 TCTGTAAACATCATTTGGCAACGCTACTTTGCAATGTTTGAAGAAACAATCTGGCGATCG 1260

1201 TCTGTAACTCATTTGGCAACGCTACCTTTGCGCATGTTTCAGAAACAACCTCGCGCATG 1260
1261 GGGTCCCATPACATGATGATGATGTTGCGACCGATTTGCCCCGACATTAATGCGAGCCAT 1320
1261 GGGTCCCATPACATGATGATGATGTTGCGACCGATTTGCCCCGACATTAATGCGAGCCAT 1320
1321 TTATACCATATATTAATCAGATCATGTTGGAATTTAATGCGCGCTCGAGCAAGAGCTTT 1380
1321 TTATACCATATATTAATCAGATCATGTTGGAATTTAATGCGCGCTCGAGCAAGAGCTTT 1380
1381 TCCCGTTGAATATGCGTCATTAACACCCCTGTAATCTGTTATGTAAGAGACAGTTT 1440
1381 TCCCGTTGAATATGCGTCATTAACACCCCTGTAATCTGTTATGTAAGAGACAGTTT 1440
1441 ATTGTCATGATATATATTTTATCTTGTCATGATGTAATCATCAGAGATTTTGAACACA 1500
1441 ATTGTCATGATATATATTTTATCTTGTCATGATGTAATCATCAGAGATTTTGAACACA 1500
1501 AGGTGCTTTCCCGCCCCCGCTGACAGCGTTTCTCTTTTCCCAACCCCAACCCCAAG 1560
1501 AGGTGCTTTCCCGCCCCCGCTGACAGCGTTTCTCTTTTCCCAACCCCAACCCCAAG 1560
1561 TTGCGGTGAAGGCGCCAGGCTCGCAGCCAACTGCGGGGCGGCGAGCCCTGCGATAGCTTC 1620
1561 TTGCGGTGAAGGCGCCAGGCTCGCAGCCAACTGCGGGGCGGCGAGCCCTGCGATAGCTTC 1620
1621 AGGTATCTCATATATATCTTTAGATGATGTAATTAATTAATTAATTAATTAATTAATTA 1680
1621 AGGTATCTCATATATATCTTTAGATGATGTAATTAATTAATTAATTAATTAATTAATTA 1680
1681 GGTGAAGATCTTTTGTATATCTCATGACCAAAATCCCTTAACTGATGTTTTCGTTCCA 1740
1681 GGTGAAGATCTTTTGTATATCTCATGACCAAAATCCCTTAACTGATGTTTTCGTTCCA 1740
1681 GGTGAAGATCTTTTGTATATCTCATGACCAAAATCCCTTAACTGATGTTTTCGTTCCA 1740
1741 CTGAGGCTCAGACCCCGTAGAAAAGATCAAGAGATCTTCTTGAGATCTTTTTCGCG 1800
1741 CTGAGGCTCAGACCCCGTAGAAAAGATCAAGAGATCTTCTTGAGATCTTTTTCGCG 1800
1801 CGTATCTGCTGCTGCAACAAAACCAACCGCTACGAGGCTGTTTTCGCGCA 1860
1801 CGTATCTGCTGCTGCAACAAAACCAACCGCTACGAGGCTGTTTTCGCGCA 1860
1801 CGTATCTGCTGCTGCAACAAAACCAACCGCTACGAGGCTGTTTTCGCGCA 1860
1861 TCAAGAGCTACCAACTTTTTCGAAAGGTACTGCTGAGAGAGCGAGATACCAAA 1920
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1861 TCAAGAGCTACCAACTTTTTCGAAAGGTACTGCTGAGAGAGCGAGATACCAAA 1920
1921 TACTGTTCTTCTGATGAGCGGTAGTTAGGCGACACTTCAAGAACTCTGAGACCGCC 1980
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1921 TACTGTTCTTCTGATGAGCGGTAGTTAGGCGACACTTCAAGAACTCTGAGACCGCC 1980
1981 TACATACCTGCTGCTGTAATCTGTTACCAAGTGGCTGCGAGTGGCGATTAAGTGTG 2040
1981 TACATACCTGCTGCTGTAATCTGTTACCAAGTGGCTGCGAGTGGCGATTAAGTGTG 2040
1981 TACATACCTGCTGCTGTAATCTGTTACCAAGTGGCTGCGAGTGGCGATTAAGTGTG 2040
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2041 TCTTACCGGGTGGAGCTCAAGAGATGTTACCGGATTAAGGCGAGCGGTGCGGCTGAAC 2100
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2101 GGGGGGTTGCTGCAACAGCCAGCTTGGAGCGAAGCACTTACCGAATGAGATCT 2160
2101 GGGGGGTTGCTGCAACAGCCAGCTTGGAGCGAAGCACTTACCGAATGAGATCT 2160
2101 GGGGGGTTGCTGCAACAGCCAGCTTGGAGCGAAGCACTTACCGAATGAGATCT 2160
2161 ACAGCGTGAAGCTTGAAGAAAGCGCCAGCTTCCGAAAGGAGAAAGCGGAGATATCC 2220
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2161 ACAGCGTGAAGCTTGAAGAAAGCGCCAGCTTCCGAAAGGAGAAAGCGGAGATATCC 2220
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2221 GGTAAAGCGAGGCTCGAAG 2280
2221 GGTAAAGCGAGGCTCGAAG 2280
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2401 GGCCTTTTGTGCTGCTTTTGTGCTCAAGTTCTTTCTGCTGCTTATCCCTGATCTGTGGA 2460
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2461 TAAAGGATTAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2520
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2521 ATAGCCATATATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2580
2521 ATAGCCATATATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2580
2581 CGCCCAAGAGCCCGCCCGCTTACGATGATGATGATGATGATGATGATGATGATGATG 2640
2581 CGCCCAAGAGCCCGCCCGCTTACGATGATGATGATGATGATGATGATGATGATGATG 2640
2641 GATATGAGGCTATATGCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700
2641 GATATGAGGCTATATGCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700
2701 GATCTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2760
2701 GATCTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2760
2761 AATCAATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 2820
2761 AATCAATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 2820
2821 TATGCTATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 2880
2821 TATGCTATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 2880
2821 TATGCTATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 2880
2881 GATATATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 2940
2881 GATATATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 2940
2881 GATATATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 2940
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2941 TACGTAATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 3000
2941 TACGTAATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 3000
3001 GACGTAATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 3060
3001 GACGTAATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 3060
3061 TTTACGTAATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 3120
3061 TTTACGTAATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 3120
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3241 GTTTGGAGATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 3300
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3301 CCAAGGATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 3360
3361 ATGCTATATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 3420
3361 ATGCTATATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 3420

OY	3421	CTATATAAGCAGAGCTCGTTTAAGGAACCGGACAGTGGCCGAGAGCGCATTCACGCTG	3480
Db	3421	CTATTATAAGCAGAGCTCGTTTAAGGAACCGGACAGTGGCCGAGAGCGCATTCACGCTG	3480
OY	3481	TTTTCGACCTCCATAGAAAGACAACCGGACCGATCCGAGCTCCGCGCCGGGACCGTGCAT	3540
Db	3481	TTTTCGACCTCCATAGAAAGACAACCGGACCGATCCGAGCTCCGCGCCGGGACCGTGCAT	3540
OY	3541	TGGAACGGGGATTTCCCGGTGCCAAGAGTGAAGTACGCTATAGACTCTATAGGCA	3600
Db	3541	TGGAACGGGGATTTCCCGGTGCCAAGAGTGAAGTACGCTATAGACTCTATAGGCA	3600
OY	3601	CACCCCTTTGGCTCTTATGCAATGCATATCTGTTTTGGCTGGGGCCATACACCCCGC	3660
Db	3601	CACCCCTTTGGCTCTTATGCAATGCATATCTGTTTTGGCTGGGGCCATACACCCCGC	3660
OY	3661	TTCCCTTATGCTATAGTGGTATAGCTTATAGCTTATAGTGGTGGTTATGACCATATAT	3720
Db	3661	TTCCCTTATGCTATAGTGGTATAGCTTATAGCTTATAGTGGTGGTTATGACCATATAT	3720
OY	3721	TGACCACTCCCTATTTGGTGAAGATCTTCCATTTACTAATCCATTAACATGGCTCTTTC	3780
Db	3721	TGACCACTCCCTATTTGGTGAAGATCTTCCATTTACTAATCCATTAACATGGCTCTTTC	3780
OY	3781	CACAACATATCTATTTGGCTATATAGCCAAATCTGTCCTTCAGAGATGACACGAGATC	3840
Db	3781	CACAACATATCTATTTGGCTATATAGCCAAATCTGTCCTTCAGAGATGACACGAGATC	3840
OY	3841	TGATATTTTACAGATAGGGGTCCCATTTATTTATTTCAAAATTCACATTAACAACAGCC	3900
Db	3841	TGATATTTTACAGATAGGGGTCCCATTTATTTATTTCAAAATTCACATTAACAACAGCC	3900
OY	3901	GTCCCCCGTCCCGCAGTTTATTTAACAATAGCGTGGATCTCAGCGCATCTCGGGT	3960
Db	3901	GTCCCCCGTCCCGCAGTTTATTTAACAATAGCGTGGATCTCAGCGCATCTCGGGT	3960
OY	3961	ACGATTTCCGGAACATGGGCTCTTCCCGGTAGCGCGGAGCTTCCACATCCGACCCCTGG	4020
Db	3961	ACGATTTCCGGAACATGGGCTCTTCCCGGTAGCGCGGAGCTTCCACATCCGACCCCTGG	4020
OY	4021	TCCCATGECCTCAGCGGCTCATATGTATGCTGCGGAGCTCTTGTCTTAAACATGAGGAGCC	4080
Db	4021	TCCCATGECCTCAGCGGCTCATATGTATGCTGCGGAGCTCTTGTCTTAAACATGAGGAGCC	4080
OY	4081	AGAATTAGGCACAGCACATATGCCACACACACATGTGTCGACACAGGCCGTGGCGGTA	4140
Db	4081	AGACTTAAAGCACAGCACATATGCCACACACACATGTGTCGACACAGGCCGTGGCGGTA	4140
OY	4141	GGGATATGTCTGMAAAATAGACTGCGGAAATGGGGCTGCGACCGGTGACCGGAGATGGAAGA	4200
Db	4141	GGGATATGTCTGMAAAATAGAGTGGGAATGGGGCTGCGACCGGTGACCGGAGATGGAAGA	4200
OY	4201	CTTAAAGCAGCGCGAGAAAGATGACGAGCAGCTGATGTTGTGTAATTCGTAAAGATCA	4260
Db	4201	CTTAAAGCAGCGCGAGAAAGATGACGAGCAGCTGATGTTGTGTAATTCGTAAAGATCA	4260
OY	4261	GAGGTAACTCCCGTTGGCGGTGCTGTAAACGGTGAAGGGCAGTGTATGCTGACGATCTC	4320
Db	4261	GAGGTAACTCCCGTTGGCGGTGCTGTAAACGGTGAAGGGCAGTGTATGCTGACGATCTC	4320
OY	4321	GTGTGTCGCGCGCGCGACCAAGACATTAATAGCTGACAGACTAAACAGACTGTCTTTC	4380
Db	4321	GTGTGTCGCGCGCGCGCGACCAAGACATTAATAGCTGACAGACTAAACAGACTGTCTTTC	4380
OY	4381	ATGGGTCTTTTCTGCAATCACCGTCCACGCGTTAATAGACTCACTAATAGGGAACCCAA	4440
Db	4381	ATGGGTCTTTTCTGCAATCACCGTCCACGCGTTAATAGACTCACTAATAGGGAACCCAA	4440
OY	4441	GCTGGCTATGCGTTTAACTTAAAGTGTGTAACGAGTCCGAGTCCAGTATGTCAGTGTGT	4500
Db	4441	GCTGGCTATGCGTTTAACTTAAAGTGTGTAACGAGTCCGAGTCCAGTATGTCAGTGTGT	4500

QY	4501	GGAAATTCGGGA-----AGAA	4516
Db	4501	GGAAATTCGGGA-----AGAA	4560
QY	4517	TGCTCCTGGCTGTTTGTACTGCTGCTGTGAGATTTCAGACCTCGCGCATTTTC	4576
Db	4561	TGTTCTTGCGCTGTTTGTATGCTTCTGTGAGATTTCAGATCTGTGATGGCATTTC	4620
QY	4577	CTAAGCCTGTGTCTCTTAAGAACTGATGGAAGGAATGTGTTCACCGTGAAGC	4636
Db	4621	CTCAGGCTGTGCTCTCTTAAGAACTGTGGGAAAAGATGTGCGCACATGTGATG	4680
QY	4637	GGGACAGAGAGCCCTGGGCGAGTTTCAGGACAGGTTCTGTGCAATATCTCTGT	4696
Db	4681	GTTATGGAGAGTCCCTGGGCGAGTTTCAGGACAGGTTCTGTGCAAGATATCTCTGT	4740
QY	4697	CCAATGCAACCTTTGGGCTCAATTTCCCTTCA CAGGGGTGAATGACCGGGAGTCTGGC	4756
Db	4741	CCAATGCAACCTGAGACCTGATGTTCCCTTCAAGGGGTGAATGACCGTGAATCTGGC	4800
QY	4757	CTTCGCTCTTTTAAATAGACCTGCGACGTGCTGTGGCAACTTCATGGAAATTCATCTGT	4816
Db	4801	CCTCTGTGTTTAAATAGACCTGCGACGTGCTGAGCAACTTCATGGTTCACATGCG	4860
QY	4817	GAAATCTGAAGTTGGCTTTTGGGGACCAATCTGCAATAGAGACGACTTGTGTAGAA	4876
Db	4861	GAAATCTGAAGTTGGATTTGGGGGCCCAATGTTGAATAGAAAGCGAGTCTTGAATAGAA	4920
QY	4877	GAAACATCTTCGATTTAGTGGCCACAGAAAGCAAAATTTTGTGCTACCTCATAG	4936
Db	4921	GAAACATTTTGTATTTAGTGTCTCGAAAAGATAGTGTCTTTTCTTACTCTCACTTAG	4980
QY	4937	CAAGCATATCCATCAGCTCAGACTATGTCAATCCCATAGGAGCCTATGGCCAAATGAAA	4996
Db	4981	CAAAACATCATATAGCTCAGTCTATGTCAATCCCAAGGACCTATGGCCAAATGAAA	5040
QY	4997	ATGATATCAACCCATGTTTAAAGCAATCAATATTTATGACCTTGTGTCTGATGAT	5056
Db	5041	ATGGGTCAACACCATCTTTAAATGATATCAACATCTACGACCTTGTGTATGATGAT	5100
QY	5057	ATTATGTCAATGAGATGCACTGTTTGGGGGAAATAGAAATCTGAGAGACATGATTTTG	5116
Db	5101	ACTATGTCTCAGGGAACACTGTTGGGGCTCTGAAATATGAGGGAACATTTGATTTTG	5160
QY	5117	CCCATGAGACCAACGCTTTTCTGGCTTGGAGATGACTCTTCTGTTCCGCTGGGAACAAG	5176
Db	5161	CCCATGAGACCAACGGGTTTCTGCTTGGACAGACTTTTCTTGTATTTGTGGGAACAAG	5220
QY	5177	AAATTCAGAACTGACAGAGATGAAAACTTCACTATTCATATTTGGAGCTGCGGGATG	5236
Db	5221	AAATTCAGAACTATACCTGGGGATGAGAACTTCACTGTTTCATCTGCGGATTTGAGAGATG	5280
QY	5237	CAGAAAAGTGTGACATTTTGCACAGATAGATACATGTGAGAGTCAACCCCAAAATCTTA	5296
Db	5281	CAGAAAAGTGTGACATTTTGCACAGATAGATCTTTGGAGGTGTGACCCCTGAANAATCTTA	5340
QY	5297	ACTTACACAGCCCAACATCTTCTCTCTTGGAGATGTGTCTGTAGGCGGATTTGAGG	5356
Db	5341	ACTTACACAGCCCAACATCTTCTCTCTCTGAGACATTTTGTAGACAGATCAGAG	5400
QY	5357	AGTACCAACAGCCATCACTTTATGACATGGAACGCCCGAGGACCTTTACCGGCTATC	5416
Db	5401	AGTATTAATAGCAATCAAGTTTATGCGATGGAACACCTGAGGGACCACTATTAAGTATC	5460
QY	5417	CTGGAATCCATGACAAATTCAGAAACCCCAAGGCTCCCTTTCAGCTGATGTGAATTTT	5476
Db	5461	CTGGAATCCATGACAAAGCCAAAACCCCAAGGCTCCCTTTCAGCAAGATGTGAATTTT	5520
QY	5477	GCTGAGATTGACCCCAATATGAATCTGTGTCCATGTGATAAGCTGCCAATTTGAGCTTTA	5536
Db	5531	GTCGAGATTGACCCCAATATGAATCTGTGTCAATGATATGAATCTGCCAATTTGAGCTTTA	5580
QY	5537	GAAATACACTGGAAGATTTGTAGTCACTTACTGGAATAGCGGATGCTCTTCAAGCA	5596


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DB 5581 GAAACACACTGGAGAGATTGGCACTCAGGAGATGAGATCCTTCTCAAGTA 5640
QY 5597 GCATGACAAATGCTTGCATCTATATGAATGAACATGTCAGGATCAGGATC 5656
DB 5641 GCATGACAAATGCTTGCATCTATATGAATGAACATGTCAGGATCAGGATC 5700
QY 5657 CCAAGCATCTATCTCTCTTCAACCATGATTTTGAAGATTTTGAAGATGAG 5716
DB 5701 CCAACGATCCATTTTCTCTTCAACCATGATTTTGAAGATTTTGAAGATGAG 5760
QY 5717 TCCGAAGGACCGCTCTCTTCAAGATTTTGAAGATTTTGAAGATTTTGAAG 5776
DB 5761 TCGGAAGGACCGCTCTCTTGAAGATTTTGAAGATTTTGAAGATTTTGAAG 5820
QY 5777 ACCGGGATCTCTATGCTCTTCTTATACAGTATGAGAAATGATTTCTTATTT 5836
DB 5821 ACAGAGACTCTTACATGATTTCTTCTTCTTACCGCTCTATAGAAATGATTTCTTCA 5880
QY 5837 CATCCAAAGATCTGGGATATGATGATGATGATGATGATGATGATGATGATGAT 5896
DB 5881 CATCCAAAGATCTGGGATATGATGATGATGATGATGATGATGATGATGATGAT 5940
QY 5897 AAGACTACATTAAGTCTTATTTGGAACAGGATGCTGATGCTGATGCTGCTG 5956
DB 5941 GAAATTAATATGAGCTTACTTATGGAACAGGATGCTGATGCTGATGCTGCTG 6000
QY 5957 CGGCGATGATGAGGAGGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 6016
DB 6001 CAGACTGATGAGGAGGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 6060
QY 6017 GTC-----ACAGAGAAAGCAAGCTTCTGAGAAAGCAAGCTTCTGAGAG 6067
DB 6061 TTGAGAAAGAAAGAAAGAAAGCAAGCTTCTGAGAAAGCAAGCTTCTGAGAG 6120
QY 6068 AAGAGATTTTCCACAGT---TGTATGAGGCTTATTAAGGCTTAGGCAATAGAT 6124
DB 6121 AAGACGATCAACAGCTTGTATGATGAGCAATCTGTGAAACATCTAGAAACAGAG 6180
QY 6125 AGGGCCAAAAAGCTGATCTGATCTTACT 6154
DB 6181 GGGACTGAAAGGTTTACTCTCACTCGACCT 6210

RESULT 3
ADD5598/c
ID ADD5598 standard; DNA; 5386 BP.
AC ADD5598;
XX
XX 15-JAN-2004 (first entry)
DE Bacterial eukaryotic expression vector pL190.
XX
XX Multicistronic eukaryotic expression vector; multiple protein expression;
KM simultaneous expression; viral internal ribosomal entry site; viral IRES;
KM chain terminator; transcription pause site; gene transfer;
KM DNA immunization; gene therapy; pL190; kanamycin resistance gene;
KM cytomegalovirus; CMV promoter/enhancer; CMV intron A;
KM encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site; cyclic;
KM circular; ds.
XX
XX ChimERIC.
OS Synthetic.
OS Human herpesvirus 5.
OS Encephalomyocarditis virus.
OS Simian virus 40.
OS Escherichia coli.
XX
XX MO2003031630-A1.
XX
XX 17-APR-2003.
XX
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PF 10-OCT-2002; 2002MO-IT000646.
XX
XX 12-OCT-2001; 2001IT-MI002110.
XX
XX (KER-) KERYOS SPA.
PI Fazio V, Rinaldi M, Sonzogni L, Tonon G, Oresini G;
DR MPI; 2003-393446/37.
XX
XX New multicistronic recombinant plasmid vectors expressing two to our
PT genes simultaneously, useful in various biotechnological applications,
PT such as gene transfer, gene therapy and in DNA immunization.
XX
XX Claim 18; SEQ ID NO 1; 52bp; English.
XX
XX The invention relates to multicistronic eukaryotic expression vectors for
CC the expression of at least two proteins of interest which may be
CC identical or different. The vectors comprise at least one eukaryotic
CC expression cassette having a promoter/enhancer sequence, an intron
CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)
CC and a chain terminator. The vectors may additionally contain a
CC transcription pause site downstream of the chain terminator. The
CC invention also encompasses eukaryotic host cells comprising a vector of
CC the invention, and the recombinant expression of two or more eukaryotic
CC proteins using host cells transformed with a vector of the invention.
CC The vectors are useful in various biotechnological applications in which
CC the simultaneous expression of two or more genes is necessary, such as
CC gene transfer protocols, DNA immunisation, or for the expression of
CC different molecules in the same cell. They may also be used in gene
CC therapy. The present sequence represents a specifically claimed vector
CC designated pL190, which comprises a cytomegalovirus (CMV)
CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)
CC IRES, an SV40 polyadenylation site and a transcription pause site, as
CC well as a kanamycin resistance gene.
XX
XX Sequence 5386 BP; 1353 A; 1307 C; 1386 G; 1340 T; 0 U; 0 Other;
SQ
XX
XX Query Match 44.9%; Score 2878.4; DB 9; Length 5386;
XX Best local Similarity 87.3%; Pred. No. 0;
XX Matches 3354; Conservative 0; Mismatches 201; Indels 285; Gaps 7;
QY 585 TTGAAAAAATCATGAGCATCAAAATGAAATGCAATTTATTCATATCAGATTATCAAT 644
DB 5381 TTGAAAAAATCATGAGCATCAAAATGAAATGCAATTTATTCATATCAGATTATCAAT 5322
QY 645 ACCATATTTTGGAAAAAGCGCTTCTGTAATGAGAGAAATCTACCGAGGAGCTTCCA 704
DB 5321 ACCATATTTTGGAAAAAGCGCTTCTGTAATGAGAGAAATCTACCGAGGAGCTTCCA 5262
QY 705 TAGATGCAAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 764
DB 5261 TAGATGCAAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5202
QY 765 TATTAATTTTCCCTGCTCAAAATAGTTATCAAGTGAAGAAATCAACATGATGAGCAG 824
DB 5201 TATTAATTTTCCCTGCTCAAAATAGTTATCAAGTGAAGAAATCAACATGATGAGCAG 5142
QY 825 TGAATTCGGTGAAGATGAGAAAGCTTATGATGATTTCTTCCAGACTGTTTCAACAGGCA 884
DB 5141 TGAATTCGGTGAAGATGAGAAAGCTTATGATGATTTCTTCCAGACTGTTTCAACAGGCA 5082
QY 885 GCCATTAGCGTCTGATCAAAATCACTGCAATCAACCAACCGTTATTTATTCGATGATG 944
DB 5081 GCCATTAGCGTCTGATCAAAATCACTGCAATCAACCAACCGTTATTTATTCGATGATG 5022
QY 945 CGCTGAGGAGAGCAAAATACCGATCGCTGTTAAAGAGCAATTAACAACAGGAATGCA 1004
DB 5021 CGCTGAGGAGAGCAAAATACCGATCGCTGTTAAAGAGCAATTAACAACAGGAATGCA 4962
QY 1005 ATGCAACCGGCGAGAGAAATCTGCCAGCGCATCAACATATTTTCACTGATCAGAGTA 1064
DB 4961 ATGCAACCGGCGAGAGAAATCTGCCAGCGCATCAACATATTTTCACTGATCAGAGTA 4902
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Db 2999 AGTACATCTACGTAATAGTATCGCTATTACATGGGATGCGGTTTGGCAGTACATCA 2940
Qy 3258 ATGGGCGTGAATAGCGTTTGACTCACGGGGATTTTCCAGTCTCACCCCATTTGAGCTCA 3117
Db 2939 ATGGGCGTGAATAGCGTTTGACTCACGGGGATTTTCCAGTCTCACCCCATTTGAGCTCA 2880
Qy 3318 ATGGGAGTTTGTGGGACCAAAATCAACGGGACCTTCCAAAATGTCTATTAACCCCG 3377
Db 2879 ATGGGAGTTTGTGGGACCAAAATCAACGGGACCTTCCAAAATGTCTATTAACCCCG 2820
Qy 3378 CCCCCCTGAGCAATGGGGGGTATGGGTATAGGTGGAGGTCTATATAGCAAGAGCTC 3437
Db 2819 CCCCATTGAGCAAAATGGGGGGTATGGGTATAGGTGGAGGTCTATATAGCAAGAGCTC 2760
Qy 3438 GTTTAGTGAACCGCTGAGATCGCTGAGAGCGCCATCCAGCCTGTTTGAACCTCATAGAA 3497
Db 2759 GTTTAGTGAACCGCTGAGATCGCTGAGAGCGCCATCCAGCCTGTTTGAACCTCATAGAA 2700
Qy 3498 GACACCGGAGCCGATCCAGCCTCCGGCCGGGACCGGTGCATTGGAAACGGGATTTCCC 3557
Db 2699 GACACCGGAGCCGATCCAGCCTCCGGCCGGGACCGGTGCATTGGAAACGGGATTTCCC 2640
Qy 3558 GTGCCAAGAGTGCATGAACCGCCCTATAGACTCTATAGGCAACCCCTTTGGCTCTTA 3617
Db 2639 GTGCCAAGAGTGCATGAACCGCCCTATAGAGCTATAGGCAACCCCTTTGGCTCTTA 2580
Qy 3618 TGCATCTATACGTTTGGCTTGGGGCTTATACACCCCGCTTCCCTTATAGT 3677
Db 2579 TGCATCTATACGTTTGGCTTGGGGCTTATACACCCCGCTTCCCTTATAGT 2520
Qy 3678 GATGTATAGCTTACCTATAGGTGGGTATTTAGCACTATTTAGCACTCCCTATTTG 3737
Db 2519 GATGTATAGCTTACCTATAGGTGGGTATTTAGCACTATTTAGCACTCCCTATTTG 2460
Qy 3738 GTACAGATATCTTCCATTAATCCATACATGGCTTTGGCAACAATCTCTATTTG 3797
Db 2459 GTACAGATATCTTCCATTAATCCATACATGGCTTTGGCAACAATCTCTATTTG 2400
Qy 3798 GCTATATGCAATCTCTGCTTCAGAGACTGACAGGACTCTGATTTTTTACAGATG 3857
Db 2399 GCTATATGCAATCTCTGCTTCAGAGACTGACAGGACTCTGATTTTTTACAGATG 2340
Qy 3858 GGGTCCCATTTATTTATTAACAATTCAATATACAACACGCGTCCCGCCGCGAG 3917
Db 2339 GGGTCCCATTTATTTATTAACAATTCAATATACAACACGCGTCCCGCCGCGAG 2280
Qy 3918 TTTTATTTAACTATAGGTGGATCTTCACAGCGAATCTCGGGTATCGTTCCGGAATGG 3977
Db 2279 TTTTATTTAACTATAGGTGGATCTTCACAGCGAATCTCGGGTATCGTTCCGGAATGG 2220
Qy 3978 GCTCTTCTCCGGTATGCGGCGGAGCTTCACATCCGAGCCTCGGTCCCATCCGAGCGG 4037
Db 2219 GCTCTTCTCCGGTATGCGGCGGAGCTTCACATCCGAGCCTCGGTCCCATCCGAGCGG 2160
Qy 4038 CTCATGCTGCTCGGAGCTCTCTGCTCTTAACAGTGAAGCCAGACTTATGGCAGCAC 4097
Db 2159 CTCATGCTGCTCGGAGCTCTCTGCTCTTAACAGTGAAGCCAGACTTATGGCAGCAC 2100
Qy 4098 AATGCCCAACCAACAGTGTGCGGCAAGGCGGTGGCGGTATGTGTCTGAAAA 4157
Db 2099 AATGCCCAACCAACAGTGTGCGGCAAGGCGGTGGCGGTATGTGTCTGAAAA 2040
Qy 4158 TTAGCTCGAGATTTGGGCTGCAACCGCTGACGAGATGAGAACTTAAAGGCAAGGAGAG 4217
Db 2039 TTAGCTCGAGATTTGGGCTGCAACCGCTGACGAGATGAGAACTTAAAGGCAAGGAGAG 1980
Qy 4218 AGAAGATGACGAGCTGATGTTGTATTTCTGATTAAGTCAAGAGTATCTCCGTGC 4277
Db 1979 AGAAGATGACGAGCTGATGTTGTATTTCTGATTAAGTCAAGAGTATCTCCGTGC 1920
Qy 4278 GGTGCTTTAAGCGTGGAGGCGAGTGTATGCTGAGCAGTACTGTTGCTCCGCGCGCGC 4337

Db 1919 GGTGCTTTAAGCGTGGAGGCGAGTGTATCTGACAGTACTGTTGCTCCGCGCGCGC 1860
Qy 4338 CACGAGACATAATAGCTGACAGACTTAACAGCTGTTCTTCCATGGGTCTTTTCTGAG 4397
Db 1859 CACGAGACATAATAGCTGACAGACTTAACAGCTGTTCTTCCATGGGTCTTTTCTGAG 1800
RESULT 4
ADD35600/c
ID ADD35600 standard; DNA; 7086 BP.
XX
AC ADD35600;
XX
DT 15-JAN-2004 (first entry)
XX
DE Tricistronic eukaryotic expression vector pL249.
XX
KW Multicistronic eukaryotic expression vector; multiple protein expression;
KW simultaneous expression; viral internal ribosomal entry site; viral IRES;
KW chain terminator; transcription pause site; gene transfer;
KW DNA immunisation; gene therapy; pL190; Kanamycin resistance gene;
KW cytomegalovirus; CMV promoter/enhancer; CMV intron A;
KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site;
KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;
KW mGB terminator; cyclic; circular; ds.
XX
XX Chimeric.
OS Synthetic.
OS Human herpesvirus 5.
OS Encephalomyocarditis virus.
OS Simian virus 40.
OS Rous sarcoma virus.
OS Oryctolagus cuniculus.
OS Escherichia coli.
XX
PN MO200301630-A1.
XX
PD 17-APR-2003.
XX
PF 10-OCT-2002; 2002MO-IT000646.
XX
PR 12-OCT-2001; 2001IT-MI002110.
XX
PA (KERY-) KERYOS SPA.
XX
PI Fazio V, Rinaldi M, Sonzogni L, Tonon G, Oresini G;
XX
DR WPI; 2003-393446/37.
XX
XX
PT New multicistronic recombinant plasmid vectors expressing two to our
PT genes simultaneously, useful in various biotechnological applications,
PT such as gene transfer, gene therapy and in DNA immunisation.
XX
PS Claim 18; SEQ ID NO 3; 52pp; English.
XX
CC The invention relates to multicistronic eukaryotic expression vectors for
CC the expression of at least two proteins of interest which may be
CC identical or different. The vectors comprise at least one eukaryotic
CC expression cassette having a promoter/enhancer sequence, an intron
CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)
CC and a chain terminator. The vectors may additionally contain a
CC transcription pause site downstream of the chain terminator. The
CC invention also encompasses eukaryotic host cells comprising a vector of
CC the invention, and the recombinant expression of two or more eukaryotic
CC proteins using host cells transformed with a vector of the invention.
CC The vectors are useful in various biotechnological applications in which
CC the simultaneous expression of two or more genes is necessary, such as
CC gene transfer protocols, DNA immunisation, or for the expression of
CC different molecules in the same cell. They may also be used in gene
CC therapy. The present sequence represents a specifically claimed vector
CC designated pL249, which comprises a cytomegalovirus (CMV)
CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)
CC IRES, an SV40 polyadenylation site, a transcription pause site, a Rous

CC sarcoma virus (RSV) promoter, rabbit beta-globin intron, and a rabbit
CC beta-globin gene m8B terminator as well as a kanamycin resistance gene.
XX
SQ Sequence 7086 BP; 1870 A; 1699 C; 1753 G; 1764 T; 0 U; 0 Other;
Query Match 44.9%; Score 2878.4; DB 9; Length 7086;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 3354; Conservative 0; Mismatches 201; Indels 285; Gaps 7;
QY 585 TTGAAAACTCATGAGCATCAAAATGAACTGCAATTTATTCATATCAGGATTATCAAT 644
DB 7081 TTGAAAACTCATGAGCATCAAAATGAACTGCAATTTATTCATATCAGGATTATCAAT 7022
QY 645 ACCATATTTTGAAGAAAAAGCGTTTCTGTATGAAAGAGAAATCAACCGAGCGCTTCCA 704
DB 7021 ACCATATTTTGAAGAAAAAGCGTTTCTGTATGAAAGAGAAATCAACCGAGCGCTTCCA 6962
QY 705 TAGATGGCAAGATCCGTGATCGGTGCGGATTCCGACTGTCGAATCAATATCAAC 764
DB 6961 TAGATGGCAAGATCCGTGATCGGTGCGGATTCCGACTGTCGAATCAATATCAAC 6902
QY 765 TATTAATTTCCCTCGTCAAAAATAGATTATCAAGTGAAGAAATCACCATGAGTGAAGAC 824
DB 6901 TATTAATTTCCCTCGTCAAAAATAGATTATCAAGTGAAGAAATCACCATGAGTGAAGAC 6842
QY 825 TGAATCCGGTGAAGTGGCAAAAGCTTATGCAATTTCTTCCAGCTTTCAACAGGCCA 884
DB 6841 TGAATCCGGTGAAGTGGCAAAAGCTTATGCAATTTCTTCCAGCTTTCAACAGGCCA 6782
QY 885 GCCATTAGCGTCCGTCATCAAAATACCTGCGATCAACCAACCGTATTCATTCGTGATTG 944
DB 6781 GCCATTAGCGTCCGTCATCAAAATACCTGCGATCAACCAACCGTATTCATTCGTGATTG 6722
QY 945 CGCCTGAGCAGACGAATAACGCGATCGCTGTAAAGACAATTTACAAACAGGAATCGA 1004
DB 6721 CGCCTGAGCAGACGAATAACGCGATCGCTGTAAAGACAATTTACAAACAGGAATCGA 6662
QY 1005 ATGCACCGGCGCAGGAACACTGCGACGCGATCAACAATTTTCACTGTAATCAGGATA 1064
DB 6661 ATGCACCGGCGCAGGAACACTGCGACGCGATCAACAATTTTCACTGTAATCAGGATA 6602
QY 1065 TTCTCTAATACCTGGAATGCTGTTTCCGCGGATGCGAGTGTGATCAATGATC 1124
DB 6601 TTCTCTAATACCTGGAATGCTGTTTCCGCGGATGCGAGTGTGATCAATGATC 6542
QY 1125 ATCAGAGTACGATTAATATGCTTATGATGTCGAAGAGCATTAATTCCTGACGCCAGT 1184
DB 6541 ATCAGAGTACGATTAATATGCTTATGATGTCGAAGAGCATTAATTCCTGACGCCAGT 6482
QY 1185 TAGCTGACCATCTCATCTGTAAATCATTTGGCAAGCGTACCTTTGCGCATGTTTCAAAA 1244
DB 6481 TAGCTGACCATCTCATCTGTAAATCATTTGGCAAGCGTACCTTTGCGCATGTTTCAAAA 6422
QY 1245 CAACCTGCGGATCCGGGCTTCCCATACATCGATTAATTTGCGCACTGATTTGCCGAC 1304
DB 6421 CAACCTGCGGATCCGGGCTTCCCATACATCGATTAATTTGCGCACTGATTTGCCGAC 6362
QY 1305 ATTATCGAGACCATTTATACCATATTAATTCAGATTCATGTTGGAATTTTAATCGCG 1364
DB 6361 ATTATCGAGACCATTTATACCATATTAATTCAGATTCATGTTGGAATTTTAATCGCG 6302
QY 1365 CCTGAGACAGACGTTTCCGTTGAATATGCTCATTAACACCCCTTGTATTAATCTGTTAT 1424
DB 6301 CCTGAGACAGACGTTTCCGTTGAATATGCTCATTAACACCCCTTGTATTAATCTGTTAT 6242
QY 1425 GTTAAAGAGAGTTTATGTTTATGATGATATTTTATCTTGTCATATGTAATCA 1484
DB 6241 GTTAAAGAGAGTTTATGTTTATGATGATATTTTATCTTGTCATATGTAATCA 6221
QY 1485 GAGATTTTGAAGACAAAGTGTTCCTCCCCCCCCCTGACGCTTCTTCTTTCCC 1544
DB 6220 ----- 6221

QY 1545 CACCCCAACCCCAAGTTCCGGTGAAGGCCAGGCTCGACGCCAAGCTGGGGCGGCGAG 1604
DB 6220 ----- 6221
QY 1605 GCCCTGCATAGCCTCAGGTTACTCATATATATCTTATGATTGATTTAAACCTTATTTT 1664
DB 6220 ----- 6221
QY 1665 AATTAAAGATCTAGTGAAGATCCTTTTGTATATCTCATAGCAAAATCCCTTAAC 1724
DB 6220 -----TCATAGCAAAATCCCTTAAC 6200
QY 1725 GTGAGTTTGGTTCCATCGAGCTTGAACCCCGGTAGAAAACCAAGATCTTCTTGAG 1784
DB 6199 GTGAGTTTGGTTCCATCGAGCTTGAACCCCGGTAGAAAACCAAGATCTTCTTGAG 6140
QY 1785 ATCTTTTCTTTCGCGGTTATCTGCTGCTTGAACCAAAAACCAACCGCTACAGCGG 1844
DB 6139 ATCTTTTCTTTCGCGGTTATCTGCTGCTTGAACCAAAAACCAACCGCTACAGCGG 6080
QY 1845 TGGTTTGGTTCCGATCAAGAGCTACAACTCTTTTCCGAAGTTACTGCTTCAGCA 1904
DB 6079 TGGTTTGGTTCCGATCAAGAGCTACAACTCTTTTCCGAAGTTACTGCTTCAGCA 6020
QY 1905 GAGCGAGATACCAATATCTGTTCTTCTAGTGAAGCGTATGTTAGGCCACACTTCAAGA 1964
DB 6019 GAGCGAGATACCAATATCTGTTCTTCTAGTGAAGCGTATGTTAGGCCACACTTCAAGA 5960
QY 1965 ACTCTGAGACCGGCTCACTACCTGCTGCTTCAATCCGTTACCAAGT---GCTGCTG 2021
DB 5959 ACTCTGAGACCGGCTCACTACCTGCTGCTTCAATCCGTTACCAAGT---GCTGCTG 5900
QY 2022 CCACTGCGCATTAAGTGTGTTCTTACCGGTTGAGACTCAAGACGATATGTTACCGGATTAAG 2081
DB 5899 CCACTGCGCATTAAGTGTGTTCTTACCGGTTGAGACTCAAGACGATATGTTACCGGATTAAG 5840
QY 2082 CGCAGGCGTGGGCTGAACGGGGGTTTCTGTCACACAGCCCACTTGAAGCAACGACT 2141
DB 5839 CGCAGGCGTGGGCTGAACGGGGGTTTCTGTCACACAGCCCACTTGAAGCAACGACT 5780
QY 2142 ACAACGAACTGAGATCTTACAGCTGAGCTATGAGAAGCGCAAGCTTCCGAAAGGA 2201
DB 5779 ACAACGAACTGAGATCTTACAGCTGAGCTATGAGAAGCGCAAGCTTCCGAAAGGA 5720
QY 2202 GAAAGCGGACAGATATCCGTTAAGCGGACGAGGTTCGAAACAGAGAGCGCACGAGGAGC 2261
DB 5719 GAAAGCGGACAGATATCCGTTAAGCGGACGAGGTTCGAAACAGAGAGCGCACGAGGAGC 5660
QY 2262 TTCCAGGGGGGAAAGCCTGATATCTTATATGCTGCTGCGGTTTCCGACCTTGACTTG 2321
DB 5659 TTCCAGGGGGGAAAGCCTGATATCTTATATGCTGCTGCGGTTTCCGACCTTGACTTG 5600
QY 2322 AGCGTGAATTTTGTATGATGCTGTCAGGGGGGAGAGCCATGGAAGAAAGCGACAGAG 2381
DB 5599 AGCGTGAATTTTGTATGATGCTGTCAGGGGGGAGAGCCATGGAAGAAAGCGACAGAG 5540
QY 2382 CGGCTTTTTCAGGTTCTTGCTGCTTGTGCTGCTTGTGCTCAATGTTCTTCTGCGT 2441
DB 5539 CGGCTTTTTCAGGTTCTTGCTGCTTGTGCTGCTTGTGCTCAATGTTCTTCTGCGT 5480
QY 2442 TATCCCTGATTTCTGATATACCGTATTAACGCGC-ATGCAATGATTAATATGTAATC 2500
DB 5479 TATCCCTGATTTCTGATATACCGTATTAACGCGCTTGTAGTGAAGTATACGCTGCGC 5420
QY 2501 AATTAGGGGTGATTGTTTATGATGCAATATATGAGTTCCGGTTTACATTAAC---TTAC 2557
DB 5419 GCAAGCAAGACCGAGCGGACGAGTCACTGACGAGAGGAGGAGGAGCGCCATATAC 5360
QY 2558 GGTAAATGGCCGCTGCTGTCAGCCGCAACGACCCCGCCATTGACGTCAATTAATGAC 2617
DB 5359 GCAATCGGCTCTCCCGCGCGTGTGCGATTAATATGACACTGACGACGAGGTTTC 5300
QY 2618 GAGATCTGATATATGTTGACAGACGATATAGGCTATATGCGCATATGAGGCGACATCAAG 2677

Db 5299 CCGACTGGAAGGGGAGTGAAGGCAAGCAATTAATGAGTTAGCTCAGTCATTAGG 5240
 Qy 2678 C-----TGGCATGAGCCCAATGCAATATGATCTATACATTAATGATG-- 2725
 Db 5239 CACCCAGGCTTACCTTATGCTTCCGGCTGTATGTTGTGGAATGTGAGGGAT 5180
 Qy 2726 --CAATTAGCCATTAATGATGATGTTATATGATCAATTAATGAGCT-----ATT 2777
 Db 5179 AACATTTTCAACAGGAACAGTATGACCATATTAAGCCAGTTGCAATGCTGCACT 5120
 Qy 2778 GGGCATTGATGATGATGATCTATATCAATAATGATCAATTAATGAGCTGATGCA 2837
 Db 5119 GGCATTGATGATGATGATCAATATATGATCAATTAATGAGCTGATGCTGATGCA 5060
 Qy 2838 TATGACCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2897
 Db 5059 CATTACCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5000
 Qy 2898 CATTAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2957
 Db 4999 CATTAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4940
 Qy 2958 CTGGCTGACCGCCCAAGCAAGCCCGCCATGATGATGATGATGATGATGATG 3017
 Db 4939 CTGGCTGACCGCCCAAGCAAGCCCGCCATGATGATGATGATGATGATGATG 4880
 Qy 3018 TAAACGCCAATAGGAGCTTTTCAATGATGATGATGATGATGATGATGATG 3077
 Db 4879 TAAACGCCAATAGGAGCTTTTCAATGATGATGATGATGATGATGATGATG 4820
 Qy 3078 ACTTGGCAGTACATCAATGATGATGATGATGATGATGATGATGATGATGATG 3137
 Db 4819 ACTTGGCAGTACATCAATGATGATGATGATGATGATGATGATGATGATGATG 4760
 Qy 3138 GTAATAGCCCGCTGATGATGATGATGATGATGATGATGATGATGATGATG 3197
 Db 4759 GTAATAGCCCGCTGATGATGATGATGATGATGATGATGATGATGATGATG 4700
 Qy 3198 AGTACATCTAATGATGATGATGATGATGATGATGATGATGATGATGATG 3257
 Db 4699 AGTACATCTAATGATGATGATGATGATGATGATGATGATGATGATGATG 4640
 Qy 3258 ATGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3317
 Db 4639 ATGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4580
 Qy 3318 ATGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3377
 Db 4579 ATGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4520
 Qy 3378 CCCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3437
 Db 4519 CCCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4460
 Qy 3438 GTTTATGAAACCGTCAATGATGATGATGATGATGATGATGATGATGATGATG 3497
 Db 4459 GTTTATGAAACCGTCAATGATGATGATGATGATGATGATGATGATGATGATG 4400
 Qy 3498 GACACCGGAGCCGATTCAGCTCCGCGCGGAGGAGCGGTGATGATGATGATG 3557
 Db 4399 GACACCGGAGCCGATTCAGCTCCGCGCGGAGGAGCGGTGATGATGATGATG 4340
 Qy 3558 GTGCGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3617
 Db 4339 GTGCGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4280
 Qy 3618 TGATGCTATATGCTTTTGGCTTGGGCGCTATACACCCCGCTTCTTATGATAGT 3677
 Db 4279 TGATGCTATATGCTTTTGGCTTGGGCGCTATACACCCCGCTTCTTATGATAGT 4220
 Qy 3678 GATGCTATATGCTTTTGGCTTGGGCGCTATACACCCCGCTTCTTATGATAGT 3737

Db 4219 GATGCTATATGCTTTTGGCTTGGGCGCTATACACCCCGCTTCTTATGATAGT 4160
 Qy 3738 GTGAGATATCTTTTCCATTAATCAATCAATCAATCAATCAATCAATCAATCAAT 3797
 Db 4159 GTGAGATATCTTTTCCATTAATCAATCAATCAATCAATCAATCAATCAATCAAT 4100
 Qy 3798 GCTATATGCAATATCTTCTGCTTCCAGAGCTGACAGAGCTCTGATTTTAAAGATG 3857
 Db 4099 GCTATATGCAATATCTTCTGCTTCCAGAGCTGACAGAGCTCTGATTTTAAAGATG 4040
 Qy 3858 GGGTCCCATTTATTTTAAATTCATCAATCAATCAATCAATCAATCAATCAATCAAT 3917
 Db 4039 GGGTCCCATTTATTTTAAATTCATCAATCAATCAATCAATCAATCAATCAATCAAT 3980
 Qy 3918 TTTTATTAATCAATGCGTGGGATCCAGCGGAATCTGGGGATGCTTCCGGAATG 3977
 Db 3979 TTTTATTAATCAATGCGTGGGATCCAGCGGAATCTGGGGATGCTTCCGGAATG 3920
 Qy 3978 GCTCTTCTCGGATGAGCGGAGCTTCCAGATCCGAGCCCTGATCCATGCTCCAGCG 4037
 Db 3919 GCTCTTCTCGGATGAGCGGAGCTTCCAGATCCGAGCCCTGATCCATGCTCCAGCG 3860
 Qy 4038 CTGATGCTGCTCGGAGCTCTTCTGCTTCAACATGATGAGGCGCACTTAAGCAAGCAG 4097
 Db 3859 CTGATGCTGCTCGGAGCTCTTCTGCTTCAACATGATGAGGCGCACTTAAGCAAGCAG 3800
 Qy 4098 AATGCCACCAACCAAGTGTGCGGCAAGGCGGAGGATGATGATGATGATGATGATG 4157
 Db 3799 AATGCCACCAACCAAGTGTGCGGCAAGGCGGAGGATGATGATGATGATGATG 3740
 Qy 4158 TGAGCTGAGATGTTGGCTCGACCGCTGACGACAGATGAGAGCTTTAAGGACGCGCAG 4217
 Db 3739 TGAGCTGAGATGTTGGCTCGACCGCTGACGACAGATGAGAGCTTTAAGGACGCGCAG 3680
 Qy 4218 AGAAGATGACAGGAGCTGATGTTGTTGATTTGATTAAGTCAAGAGTAACTCCCTTGC 4277
 Db 3679 AGAAGATGACAGGAGCTGATGTTGTTGATTTGATTAAGTCAAGAGTAACTCCCTTGC 3620
 Qy 4278 GGTGCTGTTAAGCGTGGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4337
 Db 3619 GGTGCTGTTAAGCGTGGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3560
 Qy 4338 CACCAAGATTAATAGCTGACAGACTAAGACTGTTCTTTCCATGGGCTTTTCTGACG 4397
 Db 3559 CACCAAGATTAATAGCTGACAGACTAAGACTGTTCTTTCCATGGGCTTTTCTGACG 3500
 RESULT 5
 ADD35601/c
 ID ADD35601 standard; DNA; 7334 BP.
 XX
 AC ADD35601;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Tetracistronic eukaryotic expression vector PL250.
 XX
 KW Multicistronic eukaryotic expression vector; multiple protein expression;
 KW simultaneous expression; viral internal ribosomal entry site; viral IRES;
 KW chain terminator; transcription pause site; gene transfer;
 KW DNA immunisation; gene therapy; PL190; kanamycin resistance gene;
 KW cytomegalovirus; CMV promoter/enhancer; CMV intron A;
 KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site;
 KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;
 KW hepatitis C virus; HCV IRES; mRb terminator; cyclic; circular; ds.
 XX
 OS Chimeric.
 OS Synthetic.
 OS Human herpesvirus 5.
 OS Encephalomyocarditis virus.
 OS Simian virus 40.
 OS Rous sarcoma virus.
 OS Oryzolaegus cuniculus.

QY	2022	CCAGTGGGGAATAAAGTCGTCTCTTACACGGGTTGGACTCAAGCAGATAGTACCGAATAAG	2081
Db	6147	CCAGTGGGGAATAAAGTCGTCTCTTACCGGGTTGGAATCAAGCAGATAGTAAACCGAATAAG	6088
QY	2082	CGCAGCGGTGGGCTGAACGGGGGGGTTGGTCAACAACGCCAGCTGGAGCGAAGCACT	2141
Db	6087	CGCAGCGGTGGGGCTGAACGGGGGGGTTGGTCAACAACGCCAGCTGGAGCGAAGCACT	6028
QY	2142	ACACCGAATGAATACCTTAACGCGTGAAGTGAAGAAAGCGCAAGCTTCCGAAAGGA	2201
Db	6027	ACACCGAATGAATACCTTAACGCGTGAAGTGAAGAAAGCGCAAGCTTCCGAAAGGA	5968
QY	2202	GAAAGGCGGAAGGATATCCGGTAAGCGGCAAGGATCGGAACAGAGAGCGCAGAGGAGC	2261
Db	5967	GAAAGGCGGAAGGATATCCGGTAAGCGGCAAGGATCGGAACAGAGAGCGCAGAGGAGC	5908
QY	2262	TTCCAGGGGGGAAACGCGTGGTATCTTTATAGTCTGTGGGGTTTCGCCACTGACTTG	2321
Db	5907	TTCCAGGGGGGAAACGCGTGGTATCTTTATAGTCTGTGGGGTTTCGCCACTGACTTG	5848
QY	2322	AGCGTCGATTTTGTGATGTCGTCAAGGGGGCGGAGGCTATGAAAAACCCAGCAACG	2381
Db	5847	AGCGTCGATTTTGTGATGTCGTCAAGGGGGCGGAGGCTATGAAAAACCCAGCAACG	5788
QY	2382	CGGCTTTTATACGTTCCCTGGCTTTTCTGGCTTTTGTCTACATGTTCTTCTCGGT	2441
Db	5787	CGGCTTTTATACGTTCCCTGGCTTTTCTGGCTTTTGTCTACATGTTCTTCTCGGT	5728
QY	2442	TATCCCTCGATTTCTGTGATTAACGCTATTAACCGC-AAGCATAGTTATTAATAGTAATC	2500
Db	5727	TATCCCTCGATTTCTGTGATTAACGCTATTAACCGCTTGAATGAGCTGATACCGCTGCGC	5668
QY	2501	AATTACGGGGGTCATAGTTCATAGCCCATATATGAGAGTTCCGCGTTACATAAC---TTAC	2557
Db	5667	GCAAGCGGAACGACGCGACGCGCAGTAGTGAAGAGAGAAAGCGAAGAGCGCCCAATAC	5608
QY	2558	GGTAAATGAGCCGCTGGCTGAACCGCCCAACGACCCCGCCCATTTGACGTCAATTAATGAC	2617
Db	5607	GCAAAACCCCTCTCCCGCGCGTTGGCCGATTATTAAATGACGTGGCAGACAGAGTTTC	5548
QY	2618	GAGATCTGATTAAGGTGAACAACATATGAGAGCTATATCGCCGATAGAGGCAATCAAG	2677
Db	5547	CCGACTGAAAGCGGGCAGTAGCGCAACGCAATTAATATGATTAAGTCTCACTCATTAAG	5488
QY	2678	C-----TGGACATAGGCGCAATGATATCATATCATTAATCATTAATCAATATTGG--	2725
Db	5487	CACCCCAAGGCTTTACCTTTATGCTCCGGCTCGATATGTGTGGATATTTGAGCGGAT	5428
QY	2726	--CAATTAGCCATTTAGTCAATGGTTATATAGCATTAATCAATATTGGCT-----ATT	2777
Db	5427	AACAATTTCAACAGGAAACAGCTATGACATGATTAAGCCAAAGCTTGCAATGCTCGCAGT	5368
QY	2778	GGCCATTGCATACGTTGATCTATATCATATCAATATATGATCAATTAATTTGGCTCATGTCCA	2837
Db	5367	GGCCATTGCATACGTTGATCTATATCATATATATGATCAATTAATTTGGCTCATGTCCA	5308
QY	2838	TATGACGCGCATGTTGACATTTGATTTATGACTAGTTATTAATAGTAATCAATTAACGGGT	2897
Db	5307	CATTACCCCATGTTGACATTTGATTTATGACTAGTTATTAATAGTAATCAATTAACGGGT	5248
QY	2898	CATTAGTTCAATAGCCCATATATAGAGTTCCCGTTACATATCAATTAACGGTAATAGCCCGC	2957
Db	5247	CATTAGTTCAATAGCCCATATATAGAGTTCCCGTTACATATCAATTAACGGTAATAGCCCGC	5188
QY	2958	CTGGCTGACGCGCCAAAGACCCCGCCCATTTGACGTCAATGATGACGTATGTTCCCATAG	3017
Db	5187	CTGGCTGACGCGCCAAAGACCCCGCCCATTTGACGTCAATATATAGCATATGTTCCCATAG	5128
QY	3018	TAAAGCCCAATAGGACTTTCCATTGAAGTCAATGGGTGAGATTTTACGTTAAACTGCGC	3077
Db	5127	TAAAGCCCAATAGGACTTTCCATTGAAGTCAATGGGTGAGATTTTACGTTAAACTGCGC	5068

OY	3 078	CTTTGGAGATGACATCAAGTGTATCATATATGCAAGTCCGGCCCTTATGAGTGAATGAC	3137
Db	5 067	ACTTGGAGATGACATCAAGTGTATCATATATGCAAGTGAAGTCCCTTATGAGTGAATGAC	5 008
OY	3 138	GTAATAGGACCGCTGGACATTTATGCGCAGATACATGACCTTACCGGACTTTCTACTTTGGC	3 197
Db	5 007	GTAATAGGACCGCTGGACATTTATGCGCAGATACATGACCTTATGAGACTTTCTACTTTGGC	4 948
OY	3 198	AGTACATCTACGATTTAGTCAATGCGTATTTACATGATGATGCGGTTTTGGCAAGTACCA	3 257
Db	4 947	AGTACATCTACGATTTAGTCAATGCGTATTTACATGATGATGCGGTTTTGGCAAGTACCA	4 888
OY	3 258	ATGGGCGGTGATAGCGGTTTGACTCAGCGGGATTTCCAACTCCACCCCATGAGCTCA	3 317
Db	4 887	ATGGGCGGTGATAGCGGTTTGACTCAGCGGGATTTCCAACTCCACCCCATGAGCTCA	4 828
OY	3 318	ATGGGAGTTTGTTTGGGACCCAAATACAGGGACTTTCCAAATGTGCTATTAACCCCG	3 377
Db	4 827	ATGGGAGTTTGTTTGGGACCCAAATACAGGGACTTTCCAAATGTGCTATTAACCACTCCG	4 768
OY	3 378	CCCCGTTGACGCAAAATGGGCGGTAGGCGGTGTACGGTGGGAGGTCTATATAGCAGAGCTC	3 437
Db	4 767	CCCCATGACGCAAAATGGGCGGTGTACGGTGGGAGGTCTATATTAAGCAGAGCTC	4 708
OY	3 438	GTTTATAGTAAACCGGTCAATGGCCTTGAGAGCGCATCCACGCTGTTTGGACTCCATAGAA	3 497
Db	4 707	GTTTATAGTAAACCGGTCAATGGCCTTGAGAGCGCATCCACGCTGTTTGGACTCCATAGAA	4 648
OY	3 498	GACACCGGGACCGATCCAGCCTCCGCGGGCGGGAACGGTGCATTTGAACCGGATTTCCC	3 557
Db	4 647	GACACCGGGACCGATCCAGCCTCCGCGGGCGGGAACGGTGCATTTGAACCGGATTTCCC	4 588
OY	3 558	GTGCGAAGTGAAGTAAAGTACCGGCTATAGACTCTATAGGACACACCCCTTTGGCTCTTA	3 617
Db	4 587	GTGCGAAGTGAAGTAAAGTACCGGCTATAGACTCTATAGGACACACCCCTTTGGCTCTTA	4 528
OY	3 618	TGCAATGCTATATCTGTTTTGGCTTTGGGCGCTATATACCCCGCTTCTTATGCTATAGGT	3 677
Db	4 527	TGCAATGCTATATCTGTTTTGGCTTTGGGCGCTATATACCCCGCTTCTTATGCTATAGGT	4 468
OY	3 678	GATGATATAGCTTACGCTATAGAGTGGGGTATTTGAACATATATGACACATCCGCTATTTG	3 737
Db	4 467	GATGATATAGCTTACGCTATAGAGTGGGGTATTTGAACATATATGACACATCCGCTATTTG	4 408
OY	3 738	GTGACGATACTCTTCATTACTAATCCATTAACATGCGCTCTTTGGCACAACATATCTATTTG	3 797
Db	4 407	GTGACGATACTCTTCATTACTAATCCATTAACATGCGCTCTTTGGCACAACATATCTATTTG	4 348
OY	3 798	GCTATATGCCAAATCTGTGCTTTCAGAGACTGACACGGAAGCTGTATATTTTACAGATG	3 857
Db	4 347	GCTATATGCCAAATCTGTGCTTTCAGAGACTGACACGGAAGCTGTATATTTTACAGATG	4 288
OY	3 858	GGGTCCTATTTATTTATTAACAAATTCATATACAAAGCGCGTCCCGGTCGCGCAG	3 917
Db	4 287	GGGTCCTATTTATTTATTAACAAATTCATATACAAAGCGCGTCCCGGTCGCGCAG	4 228
OY	3 918	TTTTTATTTAAACATAGCGTGGAGCTTCCAGCGAATCTCGGGTACGTTTCCGAGCATGG	3 977
Db	4 227	TTTTTATTTAAACATAGCGTGGAGCTTCCAGCGAATCTCGGGTACGTTTCCGAGCATGG	4 168
OY	3 978	GCTCTTCTCCGGTAGCGGCGGAGCTTCCATATCCAGAGCCCTGATCCATGCTTCCAGCGG	4 037
Db	4 167	GCTCTTCTCCGGTAGCGGCGGAGCTTCCATATCCAGAGCCCTGATCCATGCTTCCAGCGG	4 108
OY	4 038	CTCATATGCTGCTGGGAGCTTCTTGGCTTCTTAAACGTGAGGACGACATTTAGGACACACAC	4 097
Db	4 107	CTCATATGCTGCTGGGAGCTTCTTGGCTTCTTAAACGTGAGGACGACATTTAGGACACACAC	4 048
OY	4 098	AATGCCACACCAACAGTGTGCGGACAAAGGCGGTGGCGTATGAGTGTCTGAAAA	4 157
Db	4 047	AATGCCACACCAACAGTGTGCGGACAAAGGCGGTGGCGTATGAGTGTCTGAAAA	3 988
OY	4 158	TGACCTCGGATTTGGGCTCGACCGGCTGACGCGATGAGAAACTTAAAGCAGCGGACGA	4 217

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Db      3987  TGAGCGTGAGATTGGGCTGCGACGCTGACGACGAGTGAAGACTTAAAGCAGCGCAGCA 3928
Qy      4218  AGAAGATGCAAGCAGCTGAGTTGTTGTAATTCGTATTAAGAGTCAAGAGTTAACTCCCGTTC 4277
Db      3927  AGAAGATGCAAGCAGCTGAGTTGTTGTAATTCGTATTAAGAGTCAAGAGTTAACTCCCGTTC 3868
Qy      4278  GGTGCTGTAAACGTTGAGGCGCAGTGTAGTCTGAGCAGTACTGTTGCTGCGCGCGC 4337
Db      3867  GGTGCTGTAAACGTTGAGGCGCAGTGTAGTCTGAGCAGTACTGTTGCTGCGCGCGC 3808
Qy      4338  CACGAGCATATATAGTGAAGACTAAACAGCTGTTCTTCCATGGGCTTTTCTGAG 4397
Db      3807  CACGAGCATATATAGTGAAGACTAAACAGCTGTTCTTCCATGGGCTTTTCTGAG 3748

RESULT 6
AB259287
ID      AB259287 standard; DNA; 5089 BP.
XX
AC      AB259287;
XX
DT      10-May-2003 (first entry)
XX
DE      Plasmid pPUV2003 SEQ ID NO 2.
XX
KW      ADP-ribosylating exotoxin; immune response; immunisation; vaccine;
KM      adjuvant; cholera toxin subunit B; CTB; human cytomegalovirus; hCMV;
KW      human tissue plasminogen activator; circular; cyclic; ds.
XX
OS      Synthetic.
XX
XX      WO200304055-A2.
XX
PD      16-JAN-2003.
XX
PF      26-NOV-2001; 2001WO-US043151.
XX
PR      27-NOV-2000; 2000US-00724315.
XX
PA      (POMD-) POWDERJECT VACCINES INC.
XX
PI      Haynes JR, Arrington JB;
XX
WPI; 2003-221541/21.
XX
PT      New compositions comprising nucleic acid adjuvants, useful in
PT      immunization techniques, particularly for eliciting or enhancing an
PT      immune response against an antigen in a human.
XX
PS      Example 1; Fig 2; 143bp; English.
XX
CC      The invention relates to a composition comprising: (a) a first nucleic
CC      acid sequence that is a truncated A subunit coding region obtained or
CC      derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
CC      nucleic acid sequence that is a truncated B subunit coding region
CC      obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
CC      the truncated subunit coding regions has a 5' deletion and encodes a
CC      subunit peptide not having an amino terminal bacterial signal peptide.
CC      The composition is useful for eliciting an immune response against an
CC      antigen or for manufacturing a medicament for enhancing an immune
CC      response in a vertebrate subject (specifically a human) against an
CC      antigen. The composition is particularly useful as nucleic acid adjuvants
CC      for use in immunisation techniques. The present sequence is that of a
CC      plasmid expression vector that contains a truncated coding sequence for a
CC      cholera toxin (CT) subunit B (CTB) peptide, the human cytomegalovirus
CC      (hCMV) immediate early promoter and associated intron A sequence and the
CC      coding sequence for the signal peptide of human tissue plasminogen
CC      activator, to allow for secretion from mammalian cells of the truncated
CC      CTB expression product
XX
SQ      Sequence 5089 BP; 1268 A; 1260 C; 1267 G; 1294 T; 0 U; 0 Other;

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Query Match      37.1%; Score 2378.8; DB 7; Length 5089;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 197; Indels 41; Gaps 6;

Qy      1615  AGCCTGAGTTTACTCATATATATCTTATAGATTGATTTAAATCTTATTTTAAATTAAG 1674
Db      1067  AGACCAAGTTTATCATATATATCTTATAGATTGATTTAAATCTTATTTTAAATTAAG 1126
Qy      1675  GATCTAGTGAAGATCTTTTGTATATCTCATGACCAAAATCCCTTAACGTGATTTTC 1734
Db      1127  GATCTAGTGAAGATCTTTTGTATATCTCATGACCAAAATCCCTTAACGTGATTTTC 1186
Qy      1735  GTTCCACTGAGCGTCAAGCCCGTGAAGAAAGATCAAGATCTTCTTGAGATCTTTTTC 1794
Db      1187  GTTCCACTGAGCGTCAAGCCCGTGAAGAAAGATCAAGATCTTCTTGAGATCTTTTTC 1246
Qy      1795  TCTGCGGTATCTGCTGCTTGGCAACAAAACACACGCTACACGCGTGTGTTGTT 1854
Db      1247  TCTGCGGTATCTGCTGCTTGGCAACAAAACACACGCTACACGCGTGTGTTGTT 1306
Qy      1855  GCCGATCAAGAGCTACCAACTCTTTTCCGAAGTAACTGCTTACAGACGCGCAGAT 1914
Db      1307  GCCGATCAAGAGCTACCAACTCTTTTCCGAAGTAACTGCTTACAGACGCGCAGAT 1366
Qy      1915  ACCAATACCTGTTCTTCTAGTAGCCGTAGGCGTACACCTTCAAGAACTCTGAGC 1974
Db      1367  ACCAATACCTGTTCTTCTAGTAGGCGGTAGGCGTACACCTTCAAGAACTCTGAGC 1426
Qy      1975  ACCGCTACATATCTGCTGCTTGAATCCGTTACCAAGTGGCTGCTGACGAGTCAAA 2034
Db      1427  ACCGCTACATATCTGCTGCTTGAATCCGTTACCAAGTGGCTGCTGACGAGTCAAA 1486
Qy      2035  GTCGTGCTTACCGGGTTGAGCTCAAGACGATAGTTACCGGATAGGCGGCGGTGCGG 2094
Db      1487  GTCGTGCTTACCGGGTTGAGCTCAAGACGATAGTTACCGGATAGGCGGCGGTGCGG 1546
Qy      2095  CTGAACGGGGGGTTTCGTGCAACAGCCGCTTGGAGCGAAACGACCTACACCGAATCGAG 2154
Db      1547  CTGAACGGGGGGTTTCGTGCAACAGCCGCTTGGAGCGAAACGACCTACACCGAATCGAG 1606
Qy      2155  ATACTTACAGCTGAGCTATGAGAAAGCGCAGCTTCCGGAAGGAGAAAGCGGACAG 2214
Db      1607  ATACTTACAGCTGAGCTATGAGAAAGCGCAGCTTCCGGAAGGAGAAAGCGGACAG 1666
Qy      2215  GTATCCGTTAAGCGGACGGGTGGAACAGAGAGCGCAGCGAGGAGCTTCAGGCGGAAA 2274
Db      1667  GTATCCGTTAAGCGGACGGGTGGAACAGAGAGCGCAGCGAGGAGCTTCAGGCGGAAA 1726
Qy      2275  CGCTGTGATCTTATATAGTCTGTGCGGTTTCCGCACTCTGACTTGAAGGTGATTTT 2334
Db      1727  CGCTGTGATCTTATATAGTCTGTGCGGTTTCCGCACTCTGACTTGAAGGTGATTTT 1786
Qy      2335  GTGATGCTGTCAGGGGGGGCGAGCCTATGAGAAAACGACAGAAACGCGGCTTTTACG 2394
Db      1787  GTGATGCTGTCAGGGGGGGCGAGCCTATGAGAAAACGACAGAAACGCGGCTTTTACG 1846
Qy      2395  GTTCTGCGCCTTTTGTGCTGCGCTTTTGTCAATGTTCTTCTGCGTTATCCCTGATTC 2454
Db      1847  GTTCTGCGCCTTTTGTGCTGCGCTTTTGTCAATGTTCTTCTGCGTTATCCCTGATTC 1906
Qy      2455  TGTGATTAACCGTATTAACCGCATGCTTATGTTATTAATGTAATC-----AATTA 2505
Db      1907  TGTGATTAACCGTATTAACCGCATGCTTATGTTATTAATGTAATC-----AATTA 1966
Qy      2506  CGGGGTATTAAGTTTCAATGAGCCATATATGAGAGTTCCGCTTACATTAACGTAAATG 2565
Db      1967  CGAGCGAGGAGATCTAGTAGCAGAGAGCGAAGCGCCCAATACGCAAAACCGCTCT 2026
Qy      2566  GCCCGCTGTGCTACGCGCCCAACGACCCCGCCCATTTGACGTCAATATGACGAG----- 2620
Db      2027  CCCCGCGCTGTGCGCCCATTTATTAATGCACTGGCAGACAGAGTTTCCGACATGGAAGC 2086
Qy      2621  -----ATCGATATATAGGTAGCAGACGATATATAGGCTATATCG 2657

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PR 27-NOV-2000; 2000US-00724315.
 XX
 XX (POMD-) POMDERJECT VACCINES INC.
 XX
 XX Haynes JR, Arrington JE;
 XX
 XX WPI; 2003-221541/21.
 DR
 XX
 PT New compositions comprising nucleic acid adjuvants, useful in
 PT immunization techniques, particularly for eliciting or enhancing an
 PT immune response against an antigen in a human.
 XX
 PS Example 2; Fig 5; 143p; English.
 XX
 CC The invention relates to a composition comprising: (a) a first nucleic
 CC acid sequence that is a truncated A subunit coding region obtained or
 CC derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
 CC nucleic acid sequence that is a truncated B subunit coding region
 CC obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
 CC the truncated subunit coding regions has a 5' deletion and encodes a
 CC subunit peptide not having an amino terminal bacterial signal peptide.
 CC The composition is useful for eliciting an immune response against an
 CC antigen or for manufacturing a medicament for enhancing an immune
 CC response in a vertebrate subject (specifically a human) against an
 CC antigen. The composition is particularly useful as nucleic acid adjuvants
 CC for use in immunisation techniques. The present sequence is that of a
 CC plasmid expression vector that contains a truncated coding sequence for
 CC an E. coli heat labile enterotoxin (LT) subunit B (LTB) peptide, the
 CC human cytomegalovirus (hCMV) immediate early promoter and associated
 CC intron A sequence and the coding sequence for the signal peptide of human
 CC tissue plasminogen activator, to allow for secretion from mammalian cells
 CC of the truncated LTB expression product
 CC
 SQ Sequence 5089 BF; 1270 A; 1273 C; 1267 G; 1279 T; 0 U; 0 Other;
 Query March 37.1%; Score 2378.8; DB 7; Length 5089;
 Best Local Similarity 91.6%; Pred. No. 0;
 Matches 2598; Conservative 0; Mismatches 197; Indels 41; Gaps 6;
 QY 1615 AGCTCAGGTTACTCATATATATCTTATGATTGATTAAATCTTATTTTAAATAAG 1674
 DB 1067 AGACCAAGTTTACTCATATATATCTTATGATTGATTAAATCTTATTTTAAATAAG 1126
 QY 1675 GATCTAGTGGAAGTCTTTTGTGATATCTCATGACCAAAATCCCTTAACGTGATTTC 1734
 DB 1127 GATCTAGTGGAAGTCTTTTGTGATATCTCATGACCAAAATCCCTTAACGTGATTTC 1186
 QY 1735 GTTCCACTGAGCGGTACAGCCCGGTAGAAAAGATCAAGAGATCTTCTGAGATCCTTTT 1794
 DB 1187 GTTCCACTGAGCGGTACAGCCCGGTAGAAAAGATCAAGAGATCTTCTGAGATCCTTTT 1246
 QY 1795 TCTGCGGTATCTGCTGCTTGGCAAAACCAACCGGTACAGCGGTGTTGTT 1854
 DB 1247 TCTGCGGTATCTGCTGCTTGGCAAAACCAACCGGTACAGCGGTGTTGTT 1306
 QY 1855 GCGGATCAAGAGTACCAACTCTTTTCCGAAGGTAACTGCTTCACAGAGCGCAGAT 1914
 DB 1307 GCGGATCAAGAGTACCAACTCTTTTCCGAAGGTAACTGCTTCACAGAGCGCAGAT 1366
 QY 1915 ACCGAATATCTGTTCTTCTAGGTAGCCGTATAGGCCACCACTTCAAGAACTCTTAGC 1974
 DB 1367 ACCGAATATCTGTTCTTCTAGGTAGCCGTATAGGCCACCACTTCAAGAACTCTTAGC 1426
 QY 1975 ACCGCTACATACCTGCTGCTGTATATCTGTACAGTGGCTGCTGCAAGTGCAGTAA 2034
 DB 1427 ACCGCTACATACCTGCTGCTGTATATCTGTACAGTGGCTGCTGCAAGTGCAGTAA 1486
 QY 2035 GTGCTGCTTACCGGGTTGACCTAAGACGATAGTAAACGGAATAGGCGCGCGTGGG 2094
 DB 1487 GTGCTGCTTACCGGGTTGACCTAAGACGATAGTAAACGGAATAGGCGCGCGTGGG 1546
 QY 2095 CTGAACGGGGGTTCTGTCACACAGCCAGTTGGAGAGACGATACACCGGAACGTAG 2154

DB 1547 CTGAACGGGGGTTCTGTCACACAGCCAGCTTGGAGCGAACGACTACCGAAGTGA 1606
 QY 2155 ATACCTACAGCGGTGAGCTATGAGAAAAGCGCACGCTTCCGAAAGGAGAAAGCGGACAG 2214
 DB 1607 ATACCTACAGCGGTGAGCTATGAGAAAAGCGCACGCTTCCGAAAGGAGAAAGCGGACAG 1666
 QY 2215 GTATCCGGTAAAGGCGGAGGTCGGAACAGAGAGCGCACAGAGGAGCTTCCAGGGGAAA 2274
 DB 1667 GTATCCGGTAAAGGCGGAGGTCGGAACAGAGAGCGCACAGAGGAGCTTCCAGGGGAAA 1726
 QY 2275 CGCCTGGTATCTTATATAGTCTGCTGCGGTTTCGCACTCTGACCTTGAAGCGGTGATTTT 2334
 DB 1727 CGCCTGGTATCTTATATAGTCTGCTGCGGTTTCGCACTCTGACCTTGAAGCGGTGATTTT 1786
 QY 2335 GTGATGCTGTCAGGGGGGCGAGGCTTATGAAAAAGCCAGAACGCGGCTTTTACG 2394
 DB 1787 GTGATGCTGTCAGGGGGGCGAGGCTTATGAAAAAGCCAGAACGCGGCTTTTACG 1846
 QY 2395 GTTCCCTGCTTTTGTGCTGCGCTTTCGACAGTCTTCTCCGCTTATCCCTGATTC 2454
 DB 1847 GTTCCCTGCTTTTGTGCTGCGCTTTCGACAGTCTTCTCCGCTTATCCCTGATTC 1906
 QY 2455 TGTGATTAACCGTATTAACCGCATGATTAATTAATTAATC-----AATTA 2505
 DB 1907 TGTGATTAACCGTATTAACCGCATGATTAATTAATTAATC-----AATTA 1966
 QY 2506 CGGGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2565
 DB 1967 CGAGCGAGGAGTCAAGTAGAGCAGAGAAAGGAGCGCCAAATAGCAAAACCGCTCT 2026
 QY 2566 GCCCGCTGCTCAACCGCCCAAGACCCCGCCCATTAAGCTCAATTAATTAATTAATTA 2620
 DB 2027 CCCCAGCGCTTGGCCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2086
 QY 2621 -----ATCGATATATAGTGAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 2657
 DB 2087 GGGCAGTGAAGCGCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2146
 QY 2658 CCGATTAAGGCGCATCAAGCTGCGCAATGCGCAATGATGATGATGATGATGATGATGATG 2717
 DB 2147 ACATTTATGCTTCCGGCTGTATGTTGTGATGATGATGATGATGATGATGATGATGATGATG 2206
 QY 2718 AATATTGGCAATTAAGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2777
 DB 2207 AGGAAACAGTATGACCATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2266
 QY 2778 GGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2837
 DB 2267 GGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2326
 QY 2838 TATGACCGCATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2897
 DB 2327 TATGACCGCATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2386
 QY 2898 CATTAATTTATTAAGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2957
 DB 2387 CATTAATTTATTAAGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2446
 QY 2958 CTGGCTGACCGGCAAGACCCCGGCATTAAGCATTAATTAATTAATTAATTAATTAATTAATTA 3017
 DB 2447 CTGG-TCACCGCCCAAGACCCCGGCATTAAGCATTAATTAATTAATTAATTAATTAATTA 2505
 QY 3018 TAAAGCCATTAAGGATTTTCATTAAGTCAATGAGTGAATTAATTAATTAATTAATTAATTA 3077
 DB 2506 TAAAGCCATTAAGGATTTTCATTAAGTCAATGAGTGAATTAATTAATTAATTAATTAATTA 2565
 QY 3078 ACTTGGCAGTATCAAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3136
 DB 2566 ACTTGGCAGTATCAAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2625
 QY 3137 GGTAAATAGGCGCGCTGAGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3196
 DB 2626 GGTAAATAGGCGCGCTGAGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2685

QY 3197 CAGTACATCTACGATATTAGTCATCGCTATTACCATGTGTGAGGGTGGCAGTACACC 3256
DB 2686 CAGTACATCTACGATATTAGTCATCGCTATTACCATGTGTGAGGGTGGCAGTACACC 2745
QY 3257 AATGGCGGTGTGATAGCGGGTTGACTCAGCGGGATTTCCAAAGTCTCCACCCCATTTGAGCTC 3316
DB 2746 AATGGCGGTGTGATAGCGGGTTGACTCAGCGGGATTTCCAAAGTCTCCACCCCATTTGAGCTC 2805
QY 3317 AATGGAGATTGTTTGGACCAAAATCAACGGGACTTTCCAAATGTCGTAATTAACCCC 3376
DB 2806 AATGGAGATTGTTTGGACCAAAATCAACGGGACTTTCCAAATGTCGTAATTAACCCC 2865
QY 3377 GCCCGTTGACGCAAAATGGCGGTGAGCGTGTACGCTGAGAGGTCTATATTAAGCAGAGCT 3436
DB 2866 GCCCGTTGACGCAAAATGGCGGTGAGCGTGTACGCTGAGAGGTCTATATTAAGCAGAGCT 2925
QY 3437 CGTTTGTGACCGTCAAGTCCCTGAGAGAGCCCATCAAGCTGTTTGTGACTTCATAGA 3496
DB 2926 CGTTTGTGACCGTCAAGTCCCTGAGAGAGCCCATCAAGCTGTTTGTGACTTCATAGA 2985
QY 3497 AGACACCGGAGCGGATCAGCTCCGCGCGCGGGAAGGTGCAATTGGAACGGGATTTCCC 3556
DB 2986 AGACACCGGAGCGGATCAGCTCCGCGCGCGGGAAGGTGCAATTGGAACGGGATTTCCC 3045
QY 3557 CGTCCCAAGATGACGTAAAGTACCGCTATAGACTCTATAGGCAACCCCTTTGGCTCTT 3616
DB 3046 CGTCCCAAGATGACGTAAAGTACCGCTATAGACTCTATAGGCAACCCCTTTGGCTCTT 3105
QY 3617 ATGATGCTATATCTGTTTGGCTTGGGGCTTATACACCCCGTCTTATGCTATAGG 3676
DB 3106 ATGATGCTATATCTGTTTGGCTTGGGGCTTATACACCCCGTCTTATGCTATAGG 3164
QY 3677 TGATGATGATGCTTAGCTTAGGTTGAGGTGAGGTTATTTGACATTTATGACCACTCCCAT 3736
DB 3165 TGATGATGATGCTTAGCTTAGGTTGAGGTGAGGTTATTTGACATTTATGACCACTCCCAT 3224
QY 3737 GGTGACGATACCTTCCATTACTATATCAATACATGAGCTTTTGGCACAACTATCTAT 3796
DB 3225 GGTGACGATACCTTCCATTACTATATCAATACATGAGCTTTTGGCACAACTATCTAT 3284
QY 3797 GGTATATGCAATATCTCTCTCTGAGAGACTGACACGAGCTGTATTTTACAGAT 3856
DB 3285 GGTATATGCAATATCTCTCTCTGAGAGACTGACACGAGCTGTATTTTACAGAT 3344
QY 3857 GGGGTCCCATTTATTTTCAAAATTCATATCAACAAACGCGGCTCCCGGCGGCA 3916
DB 3345 GGGGTCCCATTTATTTTCAAAATTCATATCAACAAACGCGGCTCCCGGCGGCA 3404
QY 3917 GTTTTATTTAAACATAGCGTGGATCTCAACGCAATCTCGGTACGTTCCGGAATG 3976
DB 3405 GTTTTATTTAAACATAGCGTGGATCTCAACGCAATCTCGGTACGTTCCGGAATG 3464
QY 3977 GGCTCTTCTCGGTGAGGGGAGGCTTCCATCCAGCCCTGATCCCATGCTCCAGCG 4036
DB 3465 GGCTCTTCTCGGTGAGGGGAGGCTTCCATCCAGCCCTGATCCCATGCTCCAGCG 3524
QY 4037 GGTATGATGCTGAGGAGCTTGTGCTCTCAAGTGAAGGAGGCGGAGCTTATAGGACAGCA 4096
DB 3525 GGTATGATGCTGAGGAGCTTGTGCTCTCAAGTGAAGGAGGCGGAGCTTATAGGACAGCA 3584
QY 4097 CAATGCCACACCAACAGTGTGCGGACAAAGGCGGTGAGGTTATGTCTGTA 4156
DB 3585 CAATGCCACACCAACAGTGTGCGGACAAAGGCGGTGAGGTTATGTCTGTA 3644
QY 4157 ATGAGCTGGAAGATGGGCTGCGACCGCTGACGCAATGGAAGCTTAAAGGACGCGCAG 4216
DB 3645 ATGAGCTGGAAGATGGGCTGCGACCG- TGAACGCAATGGAAGCTTAAAGGACGCGCAG 3703
QY 4217 AAGAAGATGACGAGGAGTGTGTGATTTCTGATAAGAGTCAAGAGTAACTCCGCTG 4276
DB 3704 AAGAAGATGACGAGGAGTGTGTGATTTCTGATAAGAGTCAAGAGTAACTCCGCTG 3763

QY 4277 CCGTGTCTTTAAACGTTGAGGCGAGTGAAGTCAAGCACTACTGTTGCTGCCGCGCG 4336
DB 3764 CCGTGTCTTTAAACGTTGAGGCGAGTGAAGTCAAGCACTACTGTTGCTGCCGCGCG 3823
QY 4337 CCACGAGACATATATGCTGACAGACTGAACAGCTGTTCCATAGGGTCTTTCTGCA 4396
DB 3824 CCACGAGACATATATGCTGACAGACTGAACAGCTGTTCCATAGGGTCTTTCTGCA 3883
QY 4397 GTCAACCTCCACGCGT 4412
DB 3884 GTCAACCTCCACGCTT 3899

RESULT 8

ABZ59291

ID ABZ59291 standard; DNA; 5488 BP.

AC ABZ59291;

DT 10-MAY-2003 (first entry)

DE Plasmid pPUV2006 SEQ ID NO 6.

KW ADP-ribosylating exotoxin; immune response; immunisation; vaccine;

KW adjuvant; labile enterotoxin subunit A; LTA; human cytomegalovirus; hCMV;

KW human tissue plasmidogen activator; circular; cyclic; ds.

OS Synthetic.

XX MO2003004055-A2.

XX 16-JAN-2003.

XX 26-NOV-2001; 2001WO-US043151.

XX 27-NOV-2000; 2000US-00724315.

XX (POWDER) POWDERJECT VACCINES INC.

XX Haynes JR, Arrington JE;

XX WPI; 2003-221541/21.

XX New compositions comprising nucleic acid adjuvants, useful in

XX immunization techniques, particularly for eliciting or enhancing an

XX immune response against an antigen in a human.

XX Example 2; Fig 6; 143bp; English.

XX The invention relates to a composition comprising: (a) a first nucleic

XX acid sequence that is a truncated A subunit coding region obtained or

XX derived from a bacterial ADP-ribosylating exotoxin; and (b) a second

XX nucleic acid sequence that is a truncated B subunit coding region

XX obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of

XX the truncated subunit coding regions has a 5' deletion and encodes a

XX subunit peptide not having an amino terminal bacterial signal peptide.

XX The composition is useful for eliciting an immune response against an

XX antigen or for manufacturing a medicament for enhancing an immune

XX response in a vertebrate subject (specifically a human) against an

XX antigen. The composition is particularly useful as nucleic acid adjuvants

XX for use in immunisation techniques. The present sequence is that of a

XX plasmid expression vector that contains a truncated coding sequence for

XX an E. coli heat labile enterotoxin (LT) subunit A (LTA) peptide with a

XX deletion of the C-terminal RDEL motif, the human cytomegalovirus (hCMV)

XX immediate early promoter and associated intron A sequence and the coding

XX sequence for the signal peptide of human tissue plasmidogen activator, to

XX allow for secretion from mammalian cells of the truncated LTA expression

XX product

XX

XX

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XX

Query Match 37.1%; Score 2378.8; DB 7; Length 5488;
Best Local Similarity 91.6%; Pred. No. 0;

QY	3737	GGTGGCACTACTTTCATTACCTAAATCCATAACATGGCGCTTTGGCAGAACTATCTATT	3736
Db	3225	GGTGGCACTACTTTCATTACCTAAATCCATAACATGGCGCTTTGGCAGAACTATCTATT	3284
QY	3797	GGCTATATGCGCAATATCTGTCTCTTCCAGAGCTGACAGGACTCTGTATTTTTCACAGAT	3856
Db	3285	GGCTATATGCGCAATATCTGTCTCTTCCAGAGCTGACAGGACTCTGTATTTTTCACAGAT	3344
QY	3857	GGGGTCCCATTTATTTATTTTACAAATTCCATATACACAAGCGCGTCCCCGTCGCGCA	3916
Db	3345	GGGGTCCCATTTATTTATTTTACAAATTCCATATACACAAGCGCGTCCCCGTCGCGCA	3404
QY	3917	GTTTTATTTAAACATAGGGTGGGAGCTCTCAGCCGAATCTCGGTACGTGTTCCGGACATG	3976
Db	3405	GTTTTATTTAAACATAGGGTGGGAGCTCTCAGCCGAATCTCGGTACGTGTTCCGGACATG	3464
QY	3977	GGCTCTTCTCGGTGAGCGGCGGAGCTTCCACATCGGAGCCCTGCGCATGCTTCCAGCG	4036
Db	3465	GGCTCTTCTCGGTGAGCGGCGGAGCTTCCACATCGGAGCCCTGCGCATGCTTCCAGCG	3524
QY	4037	GCTCATGTGCTCGGTGCGAGCTTCTTGTCTTAAACAGTGAAGCCAGACTTAAAGCACA	4096
Db	3525	GCTCATGTGCTCGGTGCGAGCTTCTTGTCTTAAACAGTGAAGCCAGACTTAAAGCACA	3584
QY	4097	CAATGCCCAACCAACCAACGATGTGCGCGACAAGGCCGTGGCGGTAGGATATGTCTGA	4156
Db	3585	CAATGCCCAACCAACCAACGATGTGCGCGACAAGGCCGTGGCGGTAGGATATGTCTGA	3644
QY	4157	ATGAGCTCGAGAGATTGGGCTGCGACCGCTGACGCGAGATGAAAGATTAAAGCAGCGCAG	4216
Db	3645	ATGAGCTCGAGAGATTGGGCTGCGACCGCTGACGCGAGATGAAAGATTAAAGCAGCGCAG	3703
QY	4217	AAGAAAGATGCAAGCAGCTGAGTGTGTATTTCTGATTAAGATCAGAGGTAATCTCCGTTG	4276
Db	3704	AAGAAAGATGCAAGCAGCTGAGTGTGTATTTCTGATTAAGATCAGAGGTAATCTCCGTTG	3763
QY	4277	CGGTCTCTTTAAACGGTGAAGGGCAATGATCTTGAACGAGTACTGTTGCTGCGCGCGC	4336
Db	3764	CGGTCTCTTTAAACGGTGAAGGGCAATGATCTTGAACGAGTACTGTTGCTGCGCGCGC	3823
QY	4337	CCACGAGCATTAATAGCTGACAGACTAACAGACTGTCTCTTCCATGGGCTCTTTCGCA	4396
Db	3824	CCACGAGCATTAATAGCTGACAGACTAACAGACTGTCTCTTCCATGGGCTCTTTCGCA	3883
QY	4397	GTCACCGTCCACGCGCT 4412	
Db	3884	GTCACCGTCCACGCTT 3899	
RESULT 9			
ABZ59288			
ID	ABZ59288	standard; DNA; 5488 BP.	
AC	ABZ59288;		
XX			
XX	10-MAY-2003 (first entry)		
DT			
XX			
DE	Plasmid pRIV2006 SEQ ID NO 3.		
XX			
KW	ADP-ribosylating exotoxin; immune response; immunisation; vaccine;		
KW	adjuvant; cholera toxin subunit A; CTA; human cytomegalovirus; hCMV;		
KW	human tissue plasminogen activator; circular; cyclic; ds.		
XX			
OS	Synthetic.		
XX			
PN	WO2003004055-A2.		
PD	16-JAN-2003.		
XX			
PF	26-NOV-2001; 2001WO-US043151.		
XX			
PR	27-NOV-2000; 2000US-00724315.		
XX			

PA	'(POMD)-POMDERJECT VACCINES INC.
XX	
XX	
XX	Haynes JR, Arrington JE;
DR	WPI, 2003-221541/21.
XX	
PT	New compositions comprising nucleic acid adjuvants, useful in
PT	immunization techniques, particularly for eliciting or enhancing an
PT	immune response against an antigen in a human.
XX	
PS	Example 1; Fig 3; 143pb; English.
CC	The invention relates to a composition comprising: (a) a first nucleic
CC	acid sequence that is a truncated A subunit coding region obtained or
CC	derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
CC	nucleic acid sequence that is a truncated B subunit coding region
CC	obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
CC	the truncated subunit coding regions has a 5' deletion and encodes a
CC	subunit peptide not having an amino terminal bacterial signal peptide.
CC	The composition is useful for eliciting an immune response against an
CC	antigen or for manufacturing a medicament for enhancing an immune
CC	response in a vertebrate subject (specifically a human) against an
CC	antigen. The composition is particularly useful as nucleic acid adjuvants
CC	for use in immunisation techniques. The present sequence is that of a
CC	plasmid expression vector that contains a truncated coding sequence for a
CC	cholesterol toxin (CT) subunit A (CTA) peptide with an addition deletion at
CC	the C-terminal KDEL motif, the human cytomegalovirus (hCMV) immediate
CC	early promoter and associated intron A sequence and the coding sequence
CC	for the signal peptide of human tissue plasminogen activator, to allow
CC	for secretion from mammalian cells of the truncated CTA expression
CC	product
XX	
SQ	Sequence 5488 BP; 1367 A; 1336 C; 1370 G; 1415 T; 0 U; 0 Other;
Query Match:	37.1%; Score 2378; 8; DB 7; Length 5488;
Best Local Similarity	91.6%; Pred. No; 0; Mismatches 197; Indels 41; Gaps 6;
Matches 2359;	Conservative 0;
OY	1615 AGCCTGACGGTATCATATATATTACTTTAGATTGATTTAAACCTTCATTTTAATTTAAAG 1674
DB	1067 AGACCAATTACTCATATAATATCTTGATTTGAATTTAAAATTATTTAATTTAAAG 1126
OY	1675 GATTCAGGTGAAGATCCTTTTTGATTAATCTCATGACCAAATCCCTTAAGGTGATTTTC 1734
DB	1127 GATCAGTAGTGAAGATCCTTTTGGATTAATCTCATGACCAAATCCCTTAAGGTGATTTTC 1186
OY	1735 GTTCCACGAGCGGTGCAGACCCCCGATGAGAAGATCAAGAGATCTTCTGAGATCCTTTTT 1794
DB	1187 GTTCCACGAGCGGTGCAGACCCCCTGATGAGAAGATCAAGAGATCTTCTGAGATCCTTTTT 1246
OY	1795 TCTGCGCTAATCTGCTGCTTGCAGAAAAAACAACCCGCTACAGCGGTGTTGTTT 1854
DB	1247 TCTGCGCTAATCTGCTGCTTGCAGAAAAAACAACCCGCTACAGCGGTGTTGTTT 1306
OY	1855 GCCGGATCAAGAGCTAACCACTCTTTTTCCGAAGTAACTGCTTCAGCAGAGCGCAGAT 1914
DB	1307 GCCGGATCAAGAGCTAACCACTCTTTTTCCGAAGTAACTGCTTCAGCAGAGCGCAGAT 1366
OY	1915 ACCAAATATCTGTTCTTTCTAGAGTAGCCGCTAGTTAGGCCACACACTTCAAGAACTCTTAGC 1974
DB	1367 ACCAAATATCTGTTCTTTCTAGAGTAGCCGCTAGTTAGGCCACACACTTCAAGAACTCTTAGC 1426
OY	1975 ACCGCTTACATACCTCGCTGCTGTAATCCTGTACAGAGTGCTCTGACAGTGGCGATTA 2034
DB	1427 ACCGCTTACATACCTCGCTGCTGTAATCCTGTACAGAGTGCTCTGACAGTGGCGATTA 1486
OY	2035 GTCTGTCTTACCGGGTTTGACTCAAGACGATAGTAACTCCGATTAAGCGCAGCGTCCGG 2094
DB	1487 GTCTGTCTTACCGGGTTTGACTCAAGACGATAGTAACTCCGATTAAGCGCAGCGTCCGG 1546
OY	2095 CTGAACGGGGGTTTGTGTGCACACAGCCCACTTGGAGGAAAGCATCACCGAATGTAG 2154
DB	1547 CTGAACGGGGGTTTGTGTGCACACAGCCCACTTGGAGGAAAGCATCACCGAATGTAG 1606


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|||||
Db      3764  CGGTGCTGTTACGGTGAAGGAGGTGTACTGAGAGTACGTGTCGCGCGCG 3823
QY      4337  CCACCGAGACATATACGTGACAGACTAAGACTGTTCCCTTCCAGAGGGCTTTTCTGCA 4396
Db      3824  CCACCGAGACATATATAGCTGACAGACTAAGACTGTTCCCTTCCAGAGGGCTTTTCTGCA 3883
QY      4397  GTCACCGTCCACGCGT 4412
Db      3884  GTCACCGTCCAGCTT 3899

RESULT 10
ABZ59289
ID      ABZ59289 standard; DNA; 5500 BP.
XX
XX      ABZ59289;
AC
XX      10-MAY-2003 (first entry)
XX
XX      Plasmid pPUV2004 SEQ ID NO 4.
DE
XX      ADP-ribosylating exotoxin; immune response; immunisation; vaccine;
KM      adjuvant; labile enterotoxin subunit A; LTA; human cytomegalovirus; hCMV;
KM      human tissue plasmidogen activator; circular; cyclic; ds.
XX
XX      Synthetic.
OS
XX      MO2003004055-A2.
PN
XX      16-JAN-2003.
PD
XX      26-NOV-2001; 2001MO-US043151.
PF
XX      27-NOV-2000; 2000US-00724315.
PR
XX      (POWD-) POWDERJECT VACCINES INC.
PA
XX      Haynes JR, Arrington JE;
PI
XX      WPI; 2003-221541/21.
XX
XX      New compositions comprising nucleic acid adjuvants, useful in
PT      immunization techniques, particularly for eliciting or enhancing an
PT      immune response against an antigen in a human.
XX
XX      Example 2; Fig 4; 143pp; English.
PS
XX
XX      The invention relates to a composition comprising: (a) a first nucleic
CC      acid sequence that is a truncated A subunit coding region obtained or
CC      derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
CC      nucleic acid sequence that is a truncated B subunit coding region
CC      obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
CC      the truncated subunit coding regions has a 5' deletion and encodes a
CC      subunit peptide not having an amino terminal bacterial signal peptide.
CC      The composition is useful for eliciting an immune response against an
CC      antigen or for manufacturing a medicament for enhancing an immune
CC      response in a vertebrate subject (specifically a human) against an
CC      antigen. The composition is particularly useful as nucleic acid adjuvants
CC      for use in immunisation techniques. The present sequence is that of a
CC      plasmid expression vector that contains a truncated coding sequence for
CC      an E. coli heat labile enterotoxin (LT) subunit A (LTA) peptide, the
CC      human cytomegalovirus (hCMV) immediate early promoter and associated
CC      intron A sequence and the coding sequence for the signal peptide of human
CC      tissue plasmidogen activator, to allow for secretion from mammalian cells
CC      of the truncated LTA expression product
XX
SQ      Sequence 5500 BP; 1385 A; 1340 C; 1367 G; 1408 T; 0 U; 0 Other;
Query Match      37.1%; Score 2378.8; DB 7; Length 5500;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 197; Indels 41; Gaps 6;
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QY      1615  AGCCTCAGGTTATCTCATATATATCTTAAATTTAAACTCAATTTTAAATTTAAAG 1674
Db      1067  AGACCAAGTTTATCTCATATATATCTTAAATTTAAACTCAATTTTAAATTTAAAG 1126
QY      1675  GATCTTAGTGAAGATTCCTTTTGAATATCTCATGACCAAAATCCCTTAAACGTGATTTTC 1734
Db      1127  GATCTTAGTGAAGATTCCTTTTGAATATCTCATGACCAAAATCCCTTAAACGTGATTTTC 1186
QY      1735  GTTCCACTGAGGCTGAGACCCCGTGAAGAAAGATCAAAAGATCTTCTTGAATCTTTTTC 1794
Db      1187  GTTCCACTGAGGCTGAGACCCCGTGAAGAAAGATCAAAAGATCTTCTTGAATCTTTTTC 1246
QY      1795  TCTGCGCGTAAATCTGCTGCTTGAACCAAAAAAACCACCGTACACGCGTGTGTTTTC 1854
Db      1247  TCTGCGCGTAAATCTGCTGCTTGAACCAAAAAAACCACCGTACACGCGTGTGTTTTC 1306
QY      1855  GCCGATCAAGAGCTACCAACTTTTTCGAAAGTAACTGGCTTCAGAGAGCGAGAT 1914
Db      1307  GCCGATCAAGAGCTACCAACTTTTTCGAAAGTAACTGGCTTCAGAGAGCGAGAT 1366
QY      1915  ACCAAATACGTGTTCTTCTAGTGAAGCCGATGTAAGCCACACTTCAAGAACTGTATAC 1974
Db      1367  ACCAAATACGTGTTCTTCTAGTGAAGCCGATGTAAGCCACACTTCAAGAACTGTATAC 1426
QY      1975  ACCGCTACATACCTGCTCTGCTTAATCTGTTACCAAGTGTGCTGCTCCAGTGGCGATA 2034
Db      1427  ACCGCTACATACCTGCTCTGCTTAATCTGTTACCAAGTGTGCTGCTCCAGTGGCGATA 1486
QY      2035  GTGCGTCTTACCGGGTTGGAATCAAGAGATTAACCGGATTAAGGCGGACGCGCGGG 2094
Db      1487  GTGCGTCTTACCGGGTTGGAATCAAGAGATTAACCGGATTAAGGCGGACGCGCGGG 1546
QY      2095  CTGAACGGGGGTTGCTGACACAGCCGCTTGGAGCGAAGACCTTACACCGAACTGAG 2154
Db      1547  CTGAACGGGGGTTGCTGACACAGCCGCTTGGAGCGAAGACCTTACACCGAACTGAG 1606
QY      2155  ATACCTACAGCGTGAAGTATGAGAAAGCGCACGCTTCCGAAAGGAGAAAGCGGACAG 2214
Db      1607  ATACCTACAGCGTGAAGTATGAGAAAGCGCACGCTTCCGAAAGGAGAAAGCGGACAG 1666
QY      2215  GTATCCGTTAAGCGGAGGTTGGAACAGAGAGCGGACAGAGGAGCTTCCAGGGGAGAA 2274
Db      1667  GTATCCGTTAAGCGGAGGTTGGAACAGAGAGCGGACAGAGGAGCTTCCAGGGGAGAA 1726
QY      2275  CGCCTGATCTTTTAAAGTCTGTGCGGTTTGGCCACTGTGACTGTGAGCTGATTTT 2334
Db      1727  CGCCTGATCTTTTAAAGTCTGTGCGGTTTGGCCACTGTGACTGTGAGCTGATTTT 1786
QY      2335  GTGATGCTGTCAGAGGGGCGGAGCCTATGAGAAAAAGCGCAGCAACGCGGCTTTTACG 2394
Db      1787  GTGATGCTGTCAGAGGGGCGGAGCCTATGAGAAAAAGCGCAGCAACGCGGCTTTTACG 1846
QY      2395  GTTCCGCGCTTTTGTGTCGCTTTTGTCTCAATGTTCTTCCGCTTAATCCCGATTC 2454
Db      1847  GTTCCGCGCTTTTGTGTCGCTTTTGTCTCAATGTTCTTCCGCTTAATCCCGATTC 1906
QY      2455  TGTGATTAACCGTATTAACGCCATGATTAATTAATATATATC-----AATTA 2505
Db      1907  TGTGATTAACCGTATTAACGCCCTTTGATGATGATGATACCGCTCGCGGACGGAACGAC 1966
QY      2506  CGGAGTCAATTAAGTTCATTAAGCCCATATATATGAGTTCGCGTTACATTAACGTGAATG 2565
Db      1967  CGGAGTCAATTAAGTTCATTAAGCCCATATATATGAGTTCGCGTTACATTAACGTGAATG 2026
QY      2566  GCCCGCTGCTGATGACCGCCCAAGACCCCGCCCAATTAATGATGAGAG----- 2620
Db      2027  CCCCGCTGCTGATGACCGCCCAATTAATGATGAGTTCGCGTTACATTAACGTGAATG 2086
QY      2621  -----ATCTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2657
Db      2087  GGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2146
QY      2658  CGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2717
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[illegible]

Db	3225	GGTGACAGATACCTTTCATTACTTAATTCATACATACAGAGCTCTTGTGCACAACATCTTATT	3284
Qy	3797	GGCTAATATGCCAATATCTCTGTCTTCAGAGACTGACACGSACTCTGTATTTTAAACAGAT	3856
Db	3285	GGCTAATATGCCAATATCTCTGTCTTCAGAGACTGACACGSACTCTGTATTTTAAACAGAT	3344
Qy	3857	GGGGTCCCATTTATTTATTTTCAAAATTCACATATATCAACAAAGCGCTCCCGCTCCGCGCA	3916
Db	3345	GGGGTCCCATTTATTTATTTTCAAAATTCACATATATCAACAAAGCGCTCCCGCTCCGCGCA	3404
Qy	3917	GTTTTATTTAAACATAGACGATGAGATCTCCACGCGAATCTCGGGTACGTGTTCGCGACATG	3976
Db	3405	GTTTTATTTAAACATAGAGTGGATCTCCACGCGAATCTCGGGTACGTGTTCGCGACATG	3464
Qy	3977	GGCTCTTCTCCGGTAGCGCGGAGCTTCCACATCTCGAGCCCTGGTCCCATGCTCCACGC	4036
Db	3465	GGCTCTTCTCCGGTAGCGCGGAGCTTCCACATCTCGAGCCCTGGTCCCATGCTCCACGC	3524
Qy	4037	GCTATATGTCGCTCGGACAGCTCCTTGTCTCTTAACAGTAGAGCCAGACTTAAGGACACGCA	4096
Db	3525	GCTATATGTCGCTCGGACAGCTCCTTGTCTCTTAACAGTAGAGCCAGACTTAAGGACACGCA	3584
Qy	4097	CAATGCCACACACCAACAGATGTGCGGACAAAGCCGTGCGGTATGTCTGTGAAA	4156
Db	3585	CAATGCCACACCAACAGATGTGCGGACAAAGCCGTGCGGTATGTCTGTGAAA	3644
Qy	4157	ATGAGCTCGAGATTTGGGCTCGCACCGCTGACGCGATGGAAGACTTAAGGACAGCGCAG	4216
Db	3645	ATGAGCTCGAGATTTGGGCTCGCACCG-TGACGCGATGGAAGACTTAAGGACAGCGCAG	3703
Qy	4217	AAGAAATGCAAGGCAAGCTGAAGTTGTATTTCTGATTAAGATCAGAGGTAACTCCCGTGG	4276
Db	3704	AAGAAATGCAAGGCAAGCTGAAGTTGTATTTCTGATTAAGATCAGAGGTAACTCCCGTGG	3763
Qy	4277	CGGAGCTGTTAACGGTGGAGGGGCGAGTGAAGTCTGAGAGATACCTGTTGCTGCGCGGCGG	4336
Db	3764	CGGAGCTGTTAACGGTGGAGGGGCGAGTGAAGTCTGAGAGATACCTGTTGCTGCGCGGCGG	3823
Qy	4337	CCACCAGACATATATAGCTGACAGACTTAACAGACTGTTCTTTCCATGGGTCTTTTCTGCA	4396
Db	3824	CCACCAGACATATATATAGCTGACAGACTTAACAGACTGTTCTTTCCATGGGTCTTTTCTGCA	3883
Qy	4397	GTCACCGTCCACGCGT 4412	
Db	3884	GTCACCGTCCAAAGCTT 3899	
RESULT 11			
ABZ59286			
ID	ABZ59286	standard; DNA; 5500 BP.	
XX	AC	ABZ59286;	
XX	XX		
XX	DT	10-MAY-2003 (first entry)	
XX	DE	Plasmid pPUV2002 SEQ ID NO 1.	
XX	XX		
XX	KM	ADP-ribosylating exotoxin; immune response; immunisation; vaccine;	
XX	KM	adjuvant; cholera toxin subunit A; CTa; human cytomegalovirus; hCMV;	
XX	KM	human tissue Plasmidogen activator; circular; cyclic; ds.	
XX	OS	Synthetic.	
XX	PN	WO2003004055-A2.	
XX	PD	16-JAN-2003.	
XX	XX		
XX	PF	26-NOV-2001; 2001WO-US043151.	
XX	XX		
XX	PR	27-NOV-2000; 2000US-00724315.	
XX	XX		
XX	PA	(POWD-) POWDERJECT VACCINES INC.	
XX	XX		

QY	3257	AATGGGGGTGGATAGCGGTTTGACTCAACGGGGATTTTCCAAAGCTCCAAACCCCATTTGAAGTCC	331.6
Db	2746	AATGGGGGTGGATAGCGGTTTGACTCAACGGGGATTTTCCAAAGCTCCAAACCCCATTTGAAGTCC	280.5
QY	3317	AATGGAGATTGTTTGGACCAAAATCAACGGGACTTTCMAAATGTCGTATTAACCCC	337.6
Db	2806	AATGGAGATTGTTTGGCACAAATCAACGGGACTTTCMAAATGTCGTATTAACCCC	286.5
QY	3377	GCCCCGTTGANGCAAAATGGGGGTGATAGCGGTGTACGGTGGGAGGTCTATATTAAGCAAGCT	343.6
Db	2866	GCCCCGTTGAGCAAAATGGGGGTGATAGCGGTGTACGGTGGGAGGTCTATATTAAGCAAGCT	292.5
QY	3437	CGTTTAGTGAACCGTCAGATCGCTCGGAGACGGCATCAACGCTGTTTGAACCTCCATAGA	349.6
Db	2926	CGTTTAGTGAACCGTCAGATCGCTCGGAGACGGCATCAACGCTGTTTGAACCTCCATAGA	298.5
QY	3497	AGACACCGGGACCGATCCAGCTCCCGGGCCGGGAAACGGTGCAATTGGAAACGGGAAATCCC	355.6
Db	2986	AGACACCGGGACCGATCCAGCTCCCGGGCCGGGAAACGGTGCAATTGGAAACCGGAAATCCC	304.5
QY	3557	CGTCCCAAAGGTGACGTAAAGTACCGGCGTATAGACTATAGGACACACCCCTTGGGCTCTT	361.6
Db	3046	CGTCCCAAAGGTGACGTAAAGTACCGGCGTATAGACTATAGGACACACCCCTTGGGCTCTT	310.5
QY	3617	ATGCATGCTATACGTGTTTGGCTTGGGGCCCTATACACCCCGGCTCTTATGCTATAGG	367.6
Db	3106	ATGCATGCTATACGTGTTTGGCTTGGGGCCCTATATACACCCCGC-TCCTTATGCTATAGG	316.4
QY	3677	TGATGCTATAGCTTATAGCCTATAGGTGTGGGTATATTGACCAATTATGACCACTCCCTATTT	373.6
Db	3165	TGATGCTATAGCTTATAGCCTATAGGTGTGGGTATATTGACCAATTATGACCACTCCCTATTT	322.4
QY	3737	GGTAGCGATACCTTTCATTAATCTAATCCATACATAGGCTCTTGGCAACAACATCTCATTT	379.6
Db	3225	GGTAGCGATACCTTTCATTAATCTAATCCATACATAGGCTCTTGGCAACAACATCTCATTT	328.4
QY	3797	GGCTATATGCAATACCTCTGTCTTCAAGACCTGACACGGAACCTCTGATATTTTTCACAGAT	385.6
Db	3285	GGCTATATGCAATACCTCTGTCTTCAAGACCTGACACGGAACCTCTGATATTTTTCACAGAT	334.4
QY	3857	GGGGTCCCATTTATTTATTAACAATTTCAATATTCACATATCAACAGCGCTGCCCGTCCCGGCA	391.6
Db	3345	GGGGTCCCATTTATTTATTTATTAACAATTTCAATATTCACATATCAACAGCGCTGCCCGTCCCGGCA	340.4
QY	3917	GTTTTTATTTAAACATAGCGGTGGATCTTCCACGCGCAATCTCGGGTATCGTGTCCGCAATG	397.6
Db	3405	GTTTTTATTTAAACATAGCGGTGGATCTTCCACGCGCAATCTCGGGTATCGTGTCCGCAATG	346.4
QY	3977	GGCTCTTCTCCGGTACCGGCGGAGCTTTCACATCCGAGCCTCGTCCATGCTCCACGCG	403.6
Db	3465	GGCTCTTCTCCGGTACCGGCGGAGCTTTCACATCCGAGCCTCGTCCATGCTCCACGCG	352.4
QY	4037	GCTCATGCTGCTCGGACGACTCTTGTGCTTAAACATGTTGAGGAGGCGCACTTATAGGACACGCA	409.6
Db	3525	GCTCATGCTGCTCGGACGACTCTTGTGCTTAAACATGTTGAGGAGGCGCACTTATAGGACACGCA	358.4
QY	4097	CAATGCCACCAACCAACGATGTGCGCAACAAGCCGTGGCGGTAGAGGTATGTCTGAAA	415.6
Db	3585	CAATGCCACCAACCAACGATGTGCGCAACAAGCCGTGGCGGTAGAGGTATGTCTGAAA	364.4
QY	4157	ATGAGCTTCGAGATTGGGCTCGCACCG-TGAGCGCAAGTGGAAAGATTATAGGCAAGGCGAG	421.6
Db	3645	ATGAGCTTCGAGATTGGGCTCGCACCG-TGAGCGCAAGTGGAAAGATTATAGGCAAGGCGAG	370.3
QY	4217	AAGAAGATGACGAGCGTGAAGGTGTTGTATTTCTGAATAAGTCAAGGTTAACTCCCGTTG	427.6
Db	3704	AAGAAGATGACGAGCGTGAAGGTGTTGTATTTCTGAATAAGTCAAGGTTAACTCCCGTTG	376.3
QY	4277	CGGTGCTGTTAACGGTGGAGGGCACTGTAAGTCTGAGCAAGTACTGTTGTCTCCCGCGCG	433.6
Db	3764	CGGTGCTGTTAACGGTGGAGGGCACTGTAAGTCTGAGCAAGTACTGTTGTCTCCCGCGCG	382.3

QY	4337	CCACCACACATTAATAGCTGCAGACTAAACAGCTTCCTTCATAGGCTTTTCGCA	4396
Db	3824	CCACCACACATTAATAGCTGCAGACTAAACAGCTTCCTTCATAGGCTTTTCGCA	3883
QY	4397	GTCAACCGTCCACGGCT 4412	
Db	3884	GTCAACCGTCCACGCTT 3899	
RESULT 12			
	ADE06467		
ID	ADE06467	standard; DNA; 10466 BP.	
XX			
AC	ADE06467;		
XX			
DT	29-JAN-2004	(first entry)	
XX			
DE	Vector pGAL/IN2.		
XX			
KW	HIV infection; Anti-HIV; vaccine; ds.		
XX			
OS	Synthetic.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	99..1577	
FT		/*tag= a	
FT		/product= "Gag, with inactivating point mutations in zinc	
FT		finger packaging sequences for viral RNA"	
FT	CDS	1387..3520	
FT		/*tag= b	
FT		/product= "Pol, with inactivating point mutations in	
FT		reverse transcriptase, deletion of integrase"	
FT	exon	3645..3859	
FT		/*tag= c	
FT		/label= Tat_exon_#1	
FT	exon	3784..3859	
FT		/*tag= d	
FT	CDS	3873..4121	
FT		/label= Rev_exon_#1	
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FT	CDS	4039..6642	
FT		/product= "Vpu"	
FT		/*tag= f	
FT		/product= "Env"	
FT	exon	6205..6452	
FT		/*tag= h	
FT		/label= Rev_exon_#2	
FT	exon	6205..6295	
FT		/*tag= g	
FT		/label= Tat_exon_#2	
XX			
PN	WO2003076591-A2.		
XX			
PD	18-SEP-2003.		
XX			
PE	10-MAR-2003; 2003WO-US007177.		
XX			
PR	08-MAR-2002; 2002US-00093953.		
XX	03-JAN-2003; 2003US-00336566.		
XX			
PA	(UYEM-) UNIV EMORY.		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.		
XX			
PI	Robinson HL, Smith J, Hua J, Moss B;		
XX			
DR	WPI; 2003-731822/69.		
XX			
PT	A composition for generating an immune response against HIV comprises a		
PT	vector comprising a vaccine insert encoding one or more antigens that		
XX	elicit an immune response against HIV.		
PS	Example 16; Fig 18; 133bp; English.		
XX			

CC The present invention relates to a composition comprising a first vector
CC with a vaccine insert encoding one or more antigens that elicit an immune
CC response against HIV or a first subtype or recombinant form; and a second
CC vector comprising a vaccine insert encoding one or more antigens that
CC elicit an immune response against an HIV of a second subtype or
CC recombinant form. The composition is useful in generating an immune
CC response against HIV. The insert of the first vector or the insert of the
CC second vector comprises the sequences of two or more of: a gag, pol, env,
CC tat, rev, nef, vif, vpr or vpu gene; or their mutants, and optionally;
CC non-coding regulatory sequences of the HIV genome. At least one of the
CC two or more sequences comprises mutations that limit the encapsidation of
CC viral RNA, or a gag sequence having a mutation in one or more of the
CC sequences encoding a zinc finger. All or part of cis-acting RNA
CC encapsidation sequences have been deleted from the non-coding regulatory
CC sequences of HIV-1. The two or more sequences comprise a pol sequence
CC having a mutation that inhibits one or more of the enzymatic activities
CC of pol. The enzymatic activity is integrase activity, reverse
CC transcriptase activity or protease activity. The enzymatic activity is
CC inhibited by deleting a portion of the pol sequence or introducing one or
CC more point mutations into the pol sequence. The present sequence is one
CC such vector used to illustrate the invention.

XX Sequence 10466 BP; 3317 A; 2200 C; 2543 G; 2405 T; 0 U; 1 Other;

Query Match 31.6%; Score 2027.6; DB 9; Length 10466;
Best Local Similarity 87.4%; Pred. No. 0;
Matches 2407; Conservative 1; Mismatches 15; Indels 331; Gaps 4;

QY 1654 ACTTCATTTTAAATTTAAAGATCTAGGAAAGATCTTTTGTATATCTCATGACCA 1713
DB 8041 ACTGGCTTTCTACGTGMAAGATCTAGGAAAGATCTTTTGTATATCTCATGACCA 8100
QY 1714 AATCCCTTAAGAGATTTGTTCCATGAGGTCGACCCCGTGAAGAAAGATCAAG 1773
DB 8101 AATCCCTTAAGAGATTTGTTCCATGAGGTCGACCCCGTGAAGAAAGATCAAG 8160
QY 1774 ATCTTCTAGATCTTTTCTGCGCTAATCTGCTGCTGCAACAAAAAAACACCC 1833
DB 8161 ATCTTCTAGATCTTTTCTGCGCTAATCTGCTGCTGCAACAAAAAAACACCC 8220
QY 1834 GCTACCAAGCGGTGTTGTTGCCGATCAAGAGCTACCAACTCTTTTCCGAAGGTAC 1893
DB 8221 GCTACCAAGCGGTGTTGTTGCCGATCAAGAGCTACCAACTCTTTTCCGAAGGTAC 8280
QY 1894 TGCGTTCAGAGAGCGGATACCAATATCTGTTCTTCTAGTGAAGCGGTAGTGGCCA 1953
DB 8281 TGCGTTCAGAGAGCGGATACCAATATCTGTTCTTCTAGTGAAGCGGTAGTGGCCA 8340
QY 1954 CCACTTCAGAACTCTGTAGCAACCGCTATACCTTCGCTGCTATCCTGTTCACAGT 2013
DB 8341 CCACTTCAGAACTCTGTAGCAACCGCTATACCTTCGCTGCTATCCTGTTCACAGT 8400
QY 2014 GCGTCTGCCAGTGGCGATAGTGTCTTAAACCGGTTGAACTCAAGAGATGTTACC 2073
DB 8401 GCGTCTGCCAGTGGCGATAGTGTCTTAAACCGGTTGAACTCAAGAGATGTTACC 8460
QY 2074 GGAATAGGCGCAGCGGTGCGGGTGAACGGGGGGTGTGTGCAACAGCCGAGCTTGAAG 2133
DB 8461 GGAATAGGCGCAGCGGTGCGGGTGAACGGGGGGTGTGTGCAACAGCCGAGCTTGAAG 8520
QY 2134 AACGACTTACACCGAATGAGATACCTTACAGCGTGAAGCTTGAAGAAAGCCGCTTCC 2193
DB 8521 AACGACTTACACCGAATGAGATACCTTACAGCGTGAAGCTTGAAGAAAGCCGCTTCC 8580
QY 2194 CGAAGGAGAAAGCGGAGCAGGTATCCGGTAAAGCGGAGGCTGGAAACAGAGAGCGCAC 2253
DB 8581 CGAAGGAGAAAGCGGAGCAGGTATCCGGTAAAGCGGAGGCTGGAAACAGAGAGCGCAC 8640
QY 2254 GAAGGAGCTTCCAGGGGGGAAAGCGCTGGTATCTTTAATAGTCGTGGGTTTGGCCACT 2313
DB 8641 GAAGGAGCTTCCAGGGGGGAAAGCGCTGGTATCTTTAATAGTCGTGGGTTTGGCCACT 8700
QY 2314 CTGACTTGAAGCGTGAATTTTGTGATGCTGTCAGGGGGCGGAGCTTATGAAAAACGC 2373

DB 8701 CTGACTTGAAGCGTGAATTTTGTGATGCTGTCAGGGGGGCGGAGCTTATGAAAAACGC 8760
QY 2374 CAGCAACGGGCGCTTTTACGGTTCCTGGACCTTTTGTGCTTGTGCTCAATGTCCT 2433
DB 8761 CAGCAACGGGCGCTTTTACGGTTCCTGGACCTTTTGTGCTTGTGCTCAATGTCCT 8819
QY 2434 TCTCGGTTATCCCTGATTTCTGTGGATTAACGATTAACCGCATGATGTTATTAAT 2493
DB 8820 ----- 8819
QY 2494 AGTAAATCAATTAACGGGCTCATTAAGTTCAATAGCCATATATGAGTTCCGCTTACATAAC 2553
DB 8820 ----- 8819
QY 2554 TTAAGGTAATAGCCCGCTGGCTGACCGCCCAAGACCCCGCCCATTTGAGTCAATTA 2613
DB 8820 ----- 8819
QY 2614 TGACGAGATCTGATATAGGTGACAGACGATATAGGCTATATCGCGATAGAGCGACAT 2673
DB 8820 ----- 8819
QY 2674 CAACTGGCAATGGCCAAATGCAATTCGATCTATACATTAATCAATATTTGCCAATTAGC 2733
DB 8820 ----- 8819
QY 2734 CATATTAGCATTTGTTATATAGCATTAATCAATATTTGGCTATTTGGCCATTCATACGTT 2793
DB 8820 -----CGACAAATATTTGGCTATTTGGCCATTCATACGTT 8852
QY 2794 GTATCTATATCAAT 2853
DB 8853 GTATCTATATCAAT 8912
QY 2854 ACATTTGATTTATGACTAGTTATTAATATATATATATATATATATATATATATATATAT 2913
DB 8913 ACATTTGATTTATGACTAGTTATTAATATATATATATATATATATATATATATATATAT 8972
QY 2914 ATATATAGAGTTCCGGGTACATTAATCTTAATATATATATATATATATATATATATATAT 2973
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QY 3094 AGTGTATCATATGCAAGTCCGCCCTTATGACGTCATATGACGTAATGACGTCGCGCC 3153
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QY 3213 TAGTCATC-GCTATTAACATGATGATGATGATGATGATGATGATGATGATGATGATG 3271
DB 9273 TAGTCATCAGGCTATTAACATGATGATGATGATGATGATGATGATGATGATGATG 9332
QY 3272 CGGTTTGAATCAACGGGAGTTTCCAAATCTTCCAAATCTTCCAAATCTTCCAAATCTTCC 3331
DB 9333 CGGTTTGAATCAACGGGAGTTTCCAAATCTTCCAAATCTTCCAAATCTTCCAAATCTTCC 9392
QY 3332 TGGCAACCAATATCAACGGGAGCTTCCAAATCTTCCAAATCTTCCAAATCTTCCAAATCTT 3391
DB 9393 TGGCAACCAATATCAACGGGAGCTTCCAAATCTTCCAAATCTTCCAAATCTTCCAAATCTT 9452
QY 3392 ATGGCGGTATGAGCTGTATCGGTGGAGGTCATATATAGCAGAGCTGTTAGTGAACCGT 3451

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Db      9453 ATGGGCGGTAGGGGTGTAAGGTGGAGGTCTATATAGACAGAGCTCGTTTAGTAACCGT 9512
QY      3452 CAGATCGCTGAGAGACCCATCCAGCTGTTTGACTCCATAGAGAACAACCGGAGACCGA 3511
Db      9513 CAGATCCCTGAGAGCCCATCCAGCTGTTTGACTCCATAGAGAACAACCGGAGACCGA 9572
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Db      9693 TTTTGGCTTGGGCGCTATACACCCCGCTTCTTATGCTATAGTATAGTATAGCTTGA 9752
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Db      9753 GCCATAGGTGGGTATTTGACCATATTTGACCATCTCCCTATTTGGTGAAGACTTTTC 9812
QY      3752 CATTACTAATCCATTAATGAGCTTTTGCCACAACATATCTATTTGGCTATATGCAATA 3811
Db      9813 CATTACTAATCCATTAATGAGCTTTTGCCACAACATATCTATTTGGCTATATGCAATA 9872
QY      3812 CTCTGTCCTTCAAGAGTGAACACGAGCTGTGTATTTTTCAGAGATGGGGTCCCATTTATT 3871
Db      9873 CTCTGTCCTTCAAGAGTGAACACGAGCTGTGTATTTTTCAGAGATGGGGTCCCATTTATT 9932
QY      3872 ATTTCAAATTCATATATACAAACACCCCGTCCCCCGCGGACATTTTATTAACAT 3931
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QY      3932 AGCGTGGGATCTCCACGCGAATCTCGGGTA-CGTGTTCCGGACATGGGCTCTTCCGGT 3990
Db      9993 AGCGTGGGATCTCCACGCGAATCTCGGGTACCGGTTCCTGGACATGGGCTCTTCCGGT 10052
QY      3991 AGCGGCGGAGCTTCCACATCCGAGCCCTGTGCCATGCTCCAGCGGCTCATGGTCCGCTC 4050
Db      10053 AGCGGCGGAGCTTCCACATCCGAGCCCTGTGCCATGCTCCAGCGGCTCATGGTCCGCTC 10112
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Db      10113 GCGAGCTCTTGTCTCTTAAAGTGGAGCCGAGCTTTAGGACAGACAATGCCACCAACC 10172
QY      4111 ACCAGTGTGCGGACAGAGCCGCTGGCGGTAGGGTATGTCTGAATAATGAGCTGGAGAT 4170
Db      10173 ACCAGTGTGCGGACAGAGCCGCTGGCGGTAGGGTATGTCTGAATAATGAGCTGGAGAT 10232
QY      4171 TGGGCTGCAACCGCTGACGAGATGAGAACTTAAAGCAGCGGACAGAAAGATGACAGC 4230
Db      10233 TGGGCTGCAACCGCTGACGAGATGAGAACTTAAAGCAGCGGACAGAAAGATGACAGC 10292
QY      4231 AGCTGAGTTGTTGATTTCTGATTAAGTCAAGAGTAACTCCGTTGGCGGTGCTTTAAG 4290
Db      10293 AGCTGAGTTGTTGATTTCTGATTAAGTCAAGAGTAACTCCGTTGGCGGTGCTTTAAG 10352
QY      4291 GTGAGAGGCAAGTATGAGTCTGAGGATCTGCTGCGCGCGGACACAGACATTAAT 4350
Db      10353 GTGAGAGGCAAGTATGAGTCTGAGGATCTGCTGCGCGCGGACACAGACATTAAT 10412
QY      4351 AGCTGACAGATTAACAGACTGTTCTCTTCCATGGGCTCTTTTCTGACAGTCAACCGT 4404
Db      10413 AGCTGACAGATTAACAGACTGTTCTCTTCCATGGGCTCTTTTCTGACAGTCAACCGT 10466

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DT      29-JAN-2004 (first entry)
XX      DE      Vector pGAL/IN3.
XX      KM      HIV Infection; Anti-HIV; vaccine; ds.
XX      OS      Synthetic.
XX      FH      Key
FH      CDS      Location/Qualifiers
FT      FT      99..1577
FT      FT      /*tag= a
FT      FT      /product= "Gag, with inactivating point mutations in zinc
FT      FT      finger packaging sequences for viral RNA"
FT      CDS      1382..3520
FT      FT      /*tag= b
FT      FT      /product= "Pol, with inactivating point mutations in
FT      FT      reverse transcriptase, deletion of integrase"
FT      exon      3645..3859
FT      FT      /*tag= c
FT      FT      /label= Tat_exon_#1
FT      exon      3784..3859
FT      FT      /*tag= d
FT      FT      /label= Rev_exon_#1
FT      CDS      3873..4121
FT      FT      /*tag= e
FT      FT      /product= "Vpu"
FT      CDS      4039..6642
FT      FT      /*tag= f
FT      FT      /product= "Env"
FT      exon      6205..6452
FT      FT      /*tag= h
FT      FT      /label= Rev_exon_#2
FT      exon      6205..6295
FT      FT      /*tag= g
FT      FT      /label= Tat_exon_#2
XX      PN      MO2003076591-A2.
XX      PD      18-SEP-2003.
XX      PF      10-MAR-2003; 2003MO-US0071177.
XX      PR      08-MAR-2002; 2002US-00093953.
XX      PR      03-JAN-2003; 2003US-00336566.
XX      PA      (UYEM-) UNIV EMORY.
XX      PA      (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX      PT      Robinson HL, Smith J, Hua J, Moss B;
XX      PT      WPI; 2003-731822/69.
XX      DR      Example 15; Fig 17; 133pp; English.
XX      PT      A composition for generating an immune response against HIV comprises a
XX      PT      vector comprising a vaccine insert encoding one or more antigens that
XX      PS      elicit an immune response against HIV.
XX      PS      Example 15; Fig 17; 133pp; English.
CC      CC      The present invention relates to a composition comprising a first vector
CC      CC      with a vaccine insert encoding one or more antigens that elicit an immune
CC      CC      response against HIV or a first subtype or recombinant form; and a second
CC      CC      vector comprising a vaccine insert encoding one or more antigens that
CC      CC      elicit an immune response against an HIV of a second subtype or
CC      CC      recombinant form. The composition is useful in generating an immune
CC      CC      response against HIV. The insert of the first vector or the insert of the
CC      CC      second vector comprises the sequences of two or more of: a gag, pol, env,
CC      CC      tat, rev, nef, vif, vpr or vpu gene; or their mutants; and optionally;
CC      CC      non-coding regulatory sequences of the HIV genome. At least one of the
CC      CC      two or more sequences comprises mutations that limit the encapsidation of
CC      CC      viral RNA, or a gag sequence having a mutation in one or more of the
CC      CC      sequences encoding a zinc finger. All or part of cis-acting RNA
CC      CC      encapsidation sequences have been deleted from the non-coding regulatory
CC      CC      sequences of HIV-1. The two or more sequences comprise a pol sequence

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RESULT 13

ADE06466 standard; DNA; 10466 BP.

ADE06466;

CC having a mutation that inhibits one or more of the enzymatic activities
CC of pol. The enzymatic activity is integrase activity, reverse
CC transcriptase activity or protease activity. The enzymatic activity is
CC inhibited by deleting a portion of the pol sequence or introducing one or
CC more point mutations into the pol sequence. The present sequence is one
CC such vector used to illustrate the invention.

XX Sequence 10466 BP; 3316 A; 2205 C; 2539 G; 2405 T; 0 U; 1 Other;

Query Match 31.6%; Score 2027.6; DB 9; Length 10466;

Best Local Similarity 87.4%; Pred. No. 0;

Matches 2407; Conservative 1; Mismatches 15; Indels 331; Gaps 4;

QY 1654 ACTTCATTTTAAATTTAAAGATCTAGTGAAGATCTTTTGTATATCTCATGACCA 1713
| | | | |
DB 8041 ACTGGCTTCTACGTAAAAAGATCTAGTGAAGATCTTTTGTATATCTCATGACCA 8100
| | | | |
QY 1714 AATCCCTTAAGTGAATTTTCGTTCCACTGAGCGTCAGACCCCGTGAAGAAAGTCAAAG 1773
| | | | |
DB 8101 AATCCCTTAAGTGAATTTTCGTTCCACTGAGCGTCAGACCCCGTGAAGAAAGTCAAAG 8160
| | | | |
QY 1774 ATCTCTGAGATCTTTTTCGCGCGTATCTGCTGTGCAACAAAACCAAC 1833
| | | | |
DB 8161 ATCTCTGAGATCTTTTTCGCGCGTATCTGCTGTGCAACAAAACCAAC 8220
| | | | |
QY 1834 GCTACACGCGGTGTTTGTTCGCGGATCAAGACTAACCACTTTTTCGAAGGTAA 1893
| | | | |
DB 8221 GCTACACGCGGTGTTTGTTCGCGGATCAAGACTAACCACTTTTTCGAAGGTAA 8280
| | | | |
QY 1894 TGCGCTCAGACAGCGCGATACCAAAATCTGTTCTTCTAGTGAAGCGTATGAGCCA 1953
| | | | |
DB 8281 TGCGCTCAGACAGCGCGATACCAAAATCTGTTCTTCTAGTGAAGCGTATGAGCCA 8340
| | | | |
QY 1954 CCACCTCAAGAACTCTGTAGCACCGGCTCATCTCTGCTATCTGTTTACAGT 2013
| | | | |
DB 8341 CCACCTCAAGAACTCTGTAGCACCGGCTCATCTCTGCTATCTGTTTACAGT 8400
| | | | |
QY 2014 GGTGCTGCGACGTGCGATAGTCGTCTTACCGGTTGAGCTCAAGAGTATGAC 2073
| | | | |
DB 8401 GGTGCTGCGACGTGCGATAGTCGTCTTACCGGTTGAGCTCAAGAGTATGAC 8460
| | | | |
QY 2074 GATTAAGCGCAGCGGTGCGGCTGAACGGGGGTTCTGTGACACAGCCGCTTGAAG 2133
| | | | |
DB 8461 GATTAAGCGCAGCGGTGCGGCTGAACGGGGGTTCTGTGACACAGCCGCTTGAAG 8520
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QY 2134 AACGACTACACCGAATGATACCTACAGCGGTGAGCTATGAAGAGCGCA 2193
| | | | |
DB 8521 AACGACTACACCGAATGATACCTACAGCGGTGAGCTATGAAGAGCGCA 8580
| | | | |
QY 2194 CGAAGGAGAAAGCGCGACAGTATCCGTTAGCGGCGAGGTCGAAACAGAGAGCGCAC 2253
| | | | |
DB 8581 CGAAGGAGAAAGCGCGACAGTATCCGTTAGCGGCGAGGTCGAAACAGAGAGCGCAC 8640
| | | | |
QY 2254 GAGGAGCTTTCAGGGGGAACCGCTGTATCTTTATATGTCGTGCGGTTTCCCACT 2313
| | | | |
DB 8641 GAGGAGCTTTCAGGGGGAACCGCTGTATCTTTATATGTCGTGCGGTTTCCCACT 8700
| | | | |
QY 2314 CTGACTGAGCGATCTTTTGTATGTCGTGACGGGGGCGAGCCTATGAAAAACGC 2373
| | | | |
DB 8701 CTGACTGAGCGATCTTTTGTATGTCGTGACGGGGGCGAGCCTATGAAAAACGC 8760
| | | | |
QY 2374 CAGCAACGCGGCTTTTAAAGTTCCTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTT 2433
| | | | |
DB 8761 CAGCAACGCGGCTTTTAAAGTTCCTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTT 8819
| | | | |
QY 2434 TCTCGGTATCCCTGATTCGTGTGAATACCGTATTAACCGCATGATTAATTAAT 2493
| | | | |
DB 8820 TCTCGGTATCCCTGATTCGTGTGAATACCGTATTAACCGCATGATTAATTAAT 8819
| | | | |
QY 2494 AGTATCATTAAGGGGTATGTTGATGAGCCATATGAGTTCCGGTTACATTAAC 2553
| | | | |
DB 8820 TTTTGGCTTGGGCGCTATTAACCCCGCTTCTATGCTATAGTATGATGATTAAGCTTA 8819
| | | | |

QY 2554 TTACGGTAATGACCCCGCTGCGTGAACGCCAAGACCCCGCCATTGACGTCAATTA 2613
| | | | |
DB 8820 TTTTGGCTTGGGCGCTATTAACCCCGCTTCTATGCTATAGTATGATGATTAAGCTTA 8819
| | | | |
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| | | | |
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| | | | |
QY 2734 CATATTAGTCAATGTTATATATGATTAATTAATTTGGCTATTTGGCATTCATTC 2793
| | | | |
DB 8820 TTTTGGCTTGGGCGCTATTAACCCCGCTTCTATGCTATAGTATGATGATTAAGCTTA 8852
| | | | |
QY 2794 GATATCATTAATTAATGATTAATTTGGCTATTTGGCTATTTGGCATTCATTC 2853
| | | | |
DB 8853 GATATCATTAATTAATGATTAATTTGGCTATTTGGCTATTTGGCATTCATTC 8912
| | | | |
QY 2854 ACATTTGATTTGACTAGTTATTAATTAATTAATTTGGCTATTTGGCATTCATTC 2913
| | | | |
DB 8913 ACATTTGATTTGACTAGTTATTAATTAATTAATTTGGCTATTTGGCATTCATTC 8972
| | | | |
QY 2914 ATATATGAGTTCCGCTTACATTAATTAATTTGGCTATTTGGCATTCATTC 2973
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| | | | |
QY 3572 GTPAATGACCGCTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3631
| | | | |
DB 9633 GTPAATGACCGCTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9692
| | | | |
QY 3632 TTTTGGCTTGGGCGCTATTAACCCCGCTTCTATGCTATAGTATGATGATTAAGCTTA 3691
| | | | |

Db 8024 ACTGCTTTCTACGTGAAAAAGATCTAGTGAAAGATCTTTTTGATGATATCTCATGACAA 8083
QY 1714 AATCCCTTAACGTAAGTTTTCGTTCACTGAGAGGTGAGACCCGGTAGAAAAAGATCAAGG 1773
Db 8084 AATCCCTTAACGTAAGTTTTCGTTCACTGAGAGGTGAGACCCGGTAGAAAAAGATCAAGG 8143
QY 1774 ATCTCTTGAGATCCTTTTTTTCGCGCGTAATCTGCTGTTGCAAAACAAAACACCC 1833
Db 8144 ATCTCTTGAGATCCTTTTTTTCGCGCGTAATCTGCTGTTGCAAAACAAAACACCC 8203
QY 1834 GCTACCAAGCGGTGTTGTTTTCGCGGATCAAGAGCTAACCACTCTTTTCCAGAGTTAAC 1893
Db 8204 GCTACCAAGCGGTGTTGTTTTCGCGGATCAAGAGCTAACCACTCTTTTCCAGAGTTAAC 8263
QY 1894 TGCGCTCAGAGAGCGGAGTACCAAAATCTGTTCTTCTAGTGTAGCCGATGTTAGGCCA 1953
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QY 1954 CCACTTCAAGAACTCTGTAGCACCGGCTACATACCTCGCTCTGCTAATCCTGTTTACAGT 2013
Db 8324 CCACTTCAAGAACTCTGTAGCACCGGCTACATACCTCGCTCTGCTAATCCTGTTTACAGT 8383
QY 2014 GGTCTGCTCCAGTGGCGGATTAAGTCGTCTTACCAGGTTGGAATCAAGAGATGTTACC 2073
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QY 2074 GGATTAAGCGCAGCGGTGCGGGCTGAAACGGGGGGTGGTGACAAGCCGAGCTTTGAGCG 2133
Db 8444 GGATTAAGCGCAGCGGTGCGGGCTGAAACGGGGGGTGGTGACAAGCCGAGCTTTGAGCG 8503
QY 2134 AACGACTTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCC 2193
Db 8504 AACGACTTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCC 8563
QY 2194 CGAAGGAGAAAGCGGACAGGTAATCGGTAAGCGGAGGTGCGAAACAGAGAGCGCAC 2253
Db 8564 CGAAGGAGAAAGCGGACAGGTAATCGGTAAGCGGAGGTGCGAAACAGAGAGCGCAC 8623
QY 2254 GAGGAGCTTTCAGGGGGAAAGCGCTGATCTTTTATGATCGTGGGGTTGGCAGCCT 2313
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QY 2374 CAGCAACGGCGCTTTTACGTTCTCGGCTTTTGTGCTGCTTTGCTCAATGTTCTT 2433
Db 8744 CAGCAACGGCGCTTTTACGTTCTCGGCTTTTGTGCTGCTTTGCTCAATGTTCTT- 8802
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Db 8803 ----- 8802
QY 2674 CAACTGACACATGCGCAATGATGATCTATACATGTAATCAATATTTGCAATTAAGC 2733
Db 8803 ----- 8802
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Db 8803 -----CGACAAATATTGGCTATTGGCCATTGCAATGCTT 8835

QY 2794 GTATCTAATATCAATATATGATATTAATTTGGCTCATGTCCAAATATGACCCGCAATGTTG 2853
Db 8836 GTATCTAATATCAATATATGATATTAATTTGGCTCATGTCCAAATATGACCCGCAATGTTG 8895
QY 2854 ACATTTGATTTAGCTAGTATTATTAATGATTAATTAACGAGGTCAATTTGTTCAATGCC 2913
Db 8896 ACATTTGATTTAGCTAGTATTATTAATGATTAATTAACGAGGTCAATTTGTTCAATGCC 8955
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Db	10336	GTGAGAGGCGAGTGTAGCTGTGAGCAGTACTGCTTGCGCGCGCGCGCCACACAGACATAT	10395
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Db	10396	AGCTGACAGACTTAACAGACTGTTCTTTCCATGGGCTTTTTCGACAGTCAAC	10447
RESULT 15			
ID	ADB06462	standard; DNA; 10447 BP.	
XX	ADB06462;		
AC	29-JAN-2004	(first entry)	
XX	Vector pGAL1/C25.		
DE	HIV infection; Anti-HIV; vaccine; ds.		
XX	Synthetic.		
OS			
XX			
FT	Key	Location/Qualifiers	
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FT	CDS	4067..6628	
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FT		/+cag= h	
PT		/label= Rev_exon_#2	
FT	exon	6215..6305	
FT		/*tag= g	
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PN	MO2003076591-A2.		
PX			
PD			
PX	18-SEP-2003.		
PX			
PX	10-MAR-2003; 2003WO-US007177.		
PR	08-MAR-2002; 2002US-00093953.		
ER	03-JAN-2003; 2003US-00336566.		
PX			
PA	(UYEM-) UNIV EMORY.		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.		
PI	Robinson HL, Smith J, Hua J, Moss B;		
DR	WPI; 2003-731822/69.		
PX			
PT	A composition for generating an immune response against HIV comprises a		
PT	vector comprising a vaccine insert encoding one or more antigens that		
PT	elicit an immune response against HIV.		
PX			
PS	Example 11; Fig 13; 133pp; English.		
PX			
CC	The present invention relates to a composition comprising a first vector		
CC	with a vaccine insert encoding one or more antigens that elicit an immune		
CC	response against HIV or a first subtype or recombinant form; and a second		
CC	vector comprising a vaccine insert encoding one or more antigens that		
CC	elicit an immune response against an HIV of a second subtype or		
CC	recombinant form. The composition is useful in generating an immune		
CC	response against HIV. The insert of the first vector or the insert of the		
CC	second vector comprises the sequences of two or more of: a gag, pol, env,		
CC	tat, rev, nef, vif, vpr or vpu gene; or their mutants, and optionally;		
CC	non-coding regulatory sequences of the HIV genome. At least one of the		
CC	two or more sequences comprises mutations that limit the encapsidation of		
CC	viral RNA, or a gag sequence having a mutation in one or more of the		
CC	sequences encoding a zinc finger. All or part of cis-acting RNA		
CC	encapsidation sequences have been deleted from the non-coding regulatory		
CC	sequences of HIV-1. The two or more sequences comprise a pol sequence		
CC	having a mutation that inhibits one or more of the enzymatic activities		
CC	of pol. The enzymatic activity is integrase activity, reverse		
CC	transcriptase activity or protease activity. The enzymatic activity is		
CC	inhibited by deleting a portion of the pol sequence or introducing one or		
CC	more point mutations into the pol sequence. The present sequence is one		
CC	such vector used to illustrate the invention.		
SX			
SQ	Sequence 10447 BP; 3305 A; 2213 C; 2547 G; 2381 T; 0 U; 1 Other;		
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	Best Local Similarity	87.4%; Pred. No. 0;	
	Matches 2406; Conservative	1; Mismatches 14; Indels 331; Gaps	4;
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	8024 ACTGGCTTTCTACGTGAAGAAGATCTGAGTAAGATCTTTTATATATCTCAAGACC	8088	
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OM nucleic - nucleic search, using sw model

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Post-Processing: Minimum Match 0%

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Listing first 45 summaries

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41: em_hcgo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	2878.4	44.9	7334	AX743956	AX743956 Sequence
C 4	2378.8	37.1	5089	AX776820	AX776820 Sequence
5	2378.8	37.1	5089	AX776823	AX776823 Sequence
6	2378.8	37.1	5488	AX776821	AX776821 Sequence
7	2378.8	37.1	5488	AX776824	AX776824 Sequence
8	2378.8	37.1	5500	AX776819	AX776819 Sequence
9	2378.8	37.1	5500	AX776822	AX776822 Sequence
10	2020.8	31.5	9918	AF430344	AF430344 Synthetic
11	2008.6	31.3	5108	AX138932	AX138932 Sequence
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38	1885	29.4	1906	I17316	I17316 Sequence 1
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C 41	1855.4	29.0	5875	AX754988	AX754988 Sequence
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ALIGNMENTS

RESULT 1
AX743953/c
LOCUS AX743953 5386 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 1 from Patent WO03031630.
ACCESSION AX743953
VERSION AX743953.1 GI:30722650
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Fazio,V., Rinaldi,M., Sonzogni,L., Tonon,G. and Oresini,G.
Multi-cistronic vectors for gene transfer protocols
Patent: WO 03031630-A 1 17-APR-2003;
Keryos Spa (IT)

FEATURES

Location/Qualifiers
1..5386
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 44.9%; Score 2878.4; DB 6; Length 5386;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 3354; Conservative 0; Mismatches 201; Indels 285; Gaps 7;

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QY 645 ACCATATTTTGGAAAAAGCGTTTCTGTATATGAAAGAAAGAAATCCACCGGAGAGTTTCCA 704
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QY	2778	GGCCATTGCAACAGCTTGATCTATATCATCATATATGATCAATTTAATTTGGTCTCATGTCCAA	2837	
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Qy	4218	AGAAGATGCAGGCGAGCTGAGATTGTTGTTATTCGTATTAAGTCAAGAGTTAACTCCGTTGCG	4277					
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Qy	4338	CACCAAGCATTAATATGCTGACACAGACTAACACACTGTTCTTCCATGGGTCTTTTCTGCAG	4397					
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RESULT 3								
AX743956/c	LOCUS	AX743956	7334 bp	DNA linear PAT 14-MAY-2003				
DEFINITION	Sequence 4 from Patent WO03031630.							
ACCESSION	AX743956							
VERSION	AX743956.1	GI:30722653						
KEYWORDS	synthetic construct synthetic construct artificial sequences.							
SOURCE	1							
REFERENCE	Fazio, V., Rinaldi, M., Sonzogno, L., Tomon, G. and Orsini, G.							
AUTHORS	Multi-electronic vectors for gene transfer protocols							
JOURNAL	Patent: WO 03031630-A 4 17-APR-2003;							
FEATURES	Keyes Spa (IT)							
	Location/Qualifiers							
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ORIGIN	/organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"							
Query Match 44.9%; Score 2878.4; DB 6; Length 7334;								
Best Local Similarity 87.3%; Pred. No. 0;								
Matches 3354; Conservative 0; Mismatches 201; Indels 285; Gaps 7;								
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Db	7269	ACCAATATTTTGA	AAAGCCGTTTCTGTATGAAAGGAAACCTCACGAGGCACTTCA	7210				

QY 705 TAGGATGGCAAGATCCTGTATCGTCTGCGATTCCGACTCGTCCAAATCAATACAGACC 764
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QY 2022 CCAGTGGGATATAGTGTGCTTCAACGGGTTGAGACTCAAGAGATAGTATACCGATTAAG 2081
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QY 2082 CGCAGCGATCGGGCTGAAACGGGGGTTCTGTGACACAGCCAGCTTGAAGCGAACCT 2141
DB 6087 CGCAGCGATCGGGCTGAAACGGGGGTTCTGTGACACAGCCAGCTTGAAGCGAACCT 6028
QY 2142 ACACCGAATGAGATTCCTACAGCGTGAATGAGAAAGCGCCACGCTTCCGAAAGGA 2201
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QY 2501 AATTAAGGGGTCTATTGTTCAATGACCAATATGAGTTCCGCTTCAATAC--TTAC 2557
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DB 5427 AATTAATTTTCAACAGGAAACAGTATGACATATATGATATGATATGATATGATATGATG-- 5368
QY 2778 GGCATTTGCAATGATGATATGATATGATATGATATGATATGATATGATATGATATGATG-- 2837
DB 5367 GGCATTTGCAATGATGATATGATATGATATGATATGATATGATATGATATGATATGATG-- 5308
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ACCESSION	AX776823				
VERSION	AX776823.1 GI:32694265				
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SOURCE	unidentified				
ORGANISM	unidentified				
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AUTHORS	Haynes,J.R. and Arrington,J.E.				
TITLE	Nucleic acid adjuvants				
JOURNAL	Patent: WO 03004055-A 5 16-JAN-2003;				
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QY	1735	GTTCACTGAGGCTCAGACCCCGTAGAAAAGATCAAAGATCTTCTTGAGATCCTTTTTT	17944		
DB	1187	GTTCACTGAGGCTCAGACCCCGTAGAAAAGATCAAAGATCTTCTTGAGATCCTTTTTT	12466		
QY	1795	TCGCGCGGTAATCTGCTGCTTGCAAAACAAAACACACCGCTACACGCGGTGTGTTT	18544		

Db		1247	CTGCGGGTATCTGCTGTTCGAACAAACAAAAAACCCGCTACACAGGGTGTTGTTT	1306
OY		1855	GCCGGATCAAGAGCTTACCAACTCTTTTTCCGAAGTACTGGCTTCAGCAGAAGCGCAT	1914
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OY		1915	ACCAAATACTGTTCTTCTAGTGTAGCGGTGTTAGGCAACAATTCAAGAACTGTAGC	1974
Db		1367	ACCAAATACTGTTCTTCTAGTGTAGCGGTGTTAGGCAACAATTCAAGAACTGTAGC	1426
OY		1975	ACCGCTTAACAATCTCGCTCTGCTAATCTCGTTAACAGTGGCTGCAGTGGCGATAA	2034
Db		1427	ACCGCTTAACAATCTCGCTCTGCTAATCTCGTTAACAGTGGCTGCAGTGGCGATAA	1486
OY		2035	GTCGTGTCTTAACGGGTTTGGACTTCAGACGATAGTTAACCGATATAGCGCGCTCGG	2094
Db		1487	GTCGTGTCTTAACGGGTTTGGACTTCAGACGATAGTTAACCGATATAGCGCGCTCGG	1546
OY		2095	CTGAACGGGGGGTTCGTGCAACAAGGCCAGCTTGGACCCGAACGATCACCCGAACTGAG	2154
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OY		2718	AATATTTGGCAATTAGCCATATTAAGTCAATGGTTATATAGCAATAATATGATGGCTATTT	2777
Db		2207	AGGAAACAGCTATGACCAATGATTAACGCCAAGCTATGTGACATPAATATATATTTGGCTATT	2266
OY		2778	GGCATTTGCATACGTTGTATCTATATATATATGATCAATTTATATTTGGCTCATGTCCA	2837
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 VERSION AX776821.1 GI:32694263
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 SOURCE .
 ORGANISM unidentified
 unclassified
 unclassified.

REFERENCE
 1 Haynes, J.R. and Arrington, J.E.
 Nucleic acid adjuvants
 Patent: WO 03004055-A 3 16-JAN-2003;
 Powderject Vaccines, Inc. (US)

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Best Local Similarity 91.6%; Pred. No. 0;

Matches 2598; Conservative 0; Mismatches 197; Indels 41; Gaps 6;

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Db 1727 CGCTGCTATCTTTATAGTCTGTCGGGTTTCGCACTCTGACTTGAGCGTCAATTTT 1786
Qy 2335 GTATGCTGTCAGGGGGGCGAGGCTTAAGGAAAAAGCGACAAACCGGCTTTTACG 2394
Db 1787 GTATGCTGTCAGGGGGGCGAGGCTTAAGGAAAAAGCGACAAACCGGCTTTTACG 1846
Qy 2395 GTTCTGCGCTTTTGTGCTGAGCTTTTGTCAATGTTCTTCTGCTTATCCCTGATTC 2454
Db 1847 GTTCTGCGCTTTTGTGCTGAGCTTTTGTCAATGTTCTTCTGCTTATCCCTGATTC 1906
Qy 2455 TGTGATTAACCGTATTAACCGCATGCACTAGTATTAATGTAATC-----AATTA 2505
Db 1907 TGTGATTAACCGTATTAACCGCATGCACTAGTATTAACCGCATGCACTAGTATTA 1966
Qy 2506 CGGGGTGATTAAGTTCATAGCCCATATATGAGAGTTCCGGTTACATTAACGTTAATG 2565
Db 1967 CGAGCGCAGAGTCAAGTGAAGCAGAGAGGAGAGCGCCCAATACGCAACCGCTCT 2026
Qy 2566 GCCCGCTGCTGCTGACCGCCCAAGCAGCCCGCATTAAGTCAATATAGCAG----- 2620
Db 2027 CCCCGCGCTTTGGCCGATTCATTAATGACAGTGGCAAGAGTTCCGACTGGAAGC 2086
Qy 2621 -----ATCTGATTAAGTGAAGAGATTAATGAGCTAATTCG 2657
Db 2087 GGGCAGTGAAGCGCAACGCAATTAATGAGTGAAGTCACTCATTAAGCACCAGGCTTT 2146
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Db 2147 ACACTTATATCTTCGGCTCGATGTTGTGGAATGTGAGCGGATTAACAAATTTCCAC 2206
Qy 2718 AATATGCGCAATTAAGCATTAATGATCATGTTATATAGCATTAATCAATATGGCTATT 2777
Db 2207 AGGAAACAGCTATGACATGATTAACGCAAGCTAGTGAATTAATTAATTTGGCTATT 2266
Qy 2778 GGGCTATGCAATGTTATCTATATATATATATATATATATATATATATATATATATAT 2837
Db 2267 GGGCTATGCAATGTTATCTATATATATATATATATATATATATATATATATATATAT 2326
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Qy 2898 CATTAGTTCAATAGCCCATATATATGAGTTCGCGTTACATTAATCAATTAATGCGCCG 2957
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Qy 3317 AATGGAGTTTGTTTTGGACCAAAATCAACGGGACTTTTCAAAGTGTATTAACCC 3376
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Qy 3377 GCCCGTGAACGCAAAATGGCGGCTAGCGGCTGATGAGGCTTATTAAGCAGAGCT 3436
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Db 3345 GGGGTCCATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3404
Qy 3917 GTTTTATTAATTAATGAGGCTGCAACGCGAATCTCGGTTACGTTTCCGGAATG 3976
Db 3405 GTTTTATTAATTAATGAGGCTGCAACGCGAATCTCGGTTACGTTTCCGGAATG 3464

OY	3977	GGCTCTTCTCGGTAGCGGCGGAGGCTTCACATCCAGCCCTGTGCTCCATGCTCCAGCG	4036
Db	3465	GGCTTTTCTCGGTAGCGGCGGAGCTTCACATCCAGCCCTGTGCTCCATGCTCCAGCG	3524
OY	4037	GCTCATGTGCTCGGCGAGCTCTTGTCTCTTAACAGTGGAGGCGCAGATTAGCAGACA	4096
Db	3525	GCTCATGTGCTCGGCGAGCTCTTGTCTCTTAACAGTGGAGGCGCAGATTAGCAGACA	3584
OY	4097	CAATGCCACCAACCACAGTGTGCGGCACAAAGCCGTGGCGGTAGGGTATGTGTGAAA	4156
Db	3585	CAATGCCACCAACCACAGTGTGCGGCACAAAGCCGTGGCGGTATGTGTGAAA	3644
OY	4157	ATGAGCTCGAGATTGGGCTCGCACCGCTGACGCGATGTGAAAGACTTAAGCGAGCGGAG	4216
Db	3645	ATGAGCTCGAGATTGGGCTCGCACCG-TGACGCGATGTGAAAGACTTAAGCGAGCGGAG	3703
OY	4217	AAGAAAGATGACAGCGAGCTGAGTGTGTGATTTCTGATTAAGTCCAGAGGTAACTCCCGTTG	4276
Db	3704	AAGAAAGATGACAGCGAGCTGAGTGTGTGATTTCTGATTAAGTCCAGAGGTAACTCCCGTTG	3763
OY	4277	CGGTCGTGTAAACGGTGGAGGGCGAGTAAAGTCTGAGCAGTACTGTCGTCGCCGCGCG	4336
Db	3764	CGGTCGTGTAAACGGTGGAGGGCGAGTAAAGTCTGAGCAGTACTGTCGTCGCCGCGCG	3823
OY	4337	CCACCAGACATTAATAGCTGACAGACTTAAACAAGCTGTTCTTTTCCATGCGTCTTTTCTGCA	4396
Db	3824	CCACCAGACATTAATAGCTGACAGACTTAAACAAGCTGTTCTTTTCCATGCGTCTTTTCTGCA	3883
OY	4397	GTCACCGTCCACGCGCT 4412	
Db	3884	GTCACCGTCCACGCTT 3899	

QY	1795	TCGCGGGTATCTGCGCTGTGGCAAAACAAAAAACACCGCTACACGGGTGGTTTGT	1854
Db	1247	TCGCGGGTATCTGCTGCTTGGCAACAAAAAACACCGCTACACGGGTGGTTTGT	1306
QY	1855	GCCGGATCAAGACTACCAACTCTTTTCCGAAGTAACTGGCTTCAGCAGACGCAGAT	1914
Db	1307	GCCGGATCAAGACTACCAACTCTTTTCCGAAGTAACTGGCTTCAGCAGACGCAGAT	1366
QY	1915	ACCAATATCATGTTCTTCTAGTGTAGCGGTATAGGCACCACTTCAAGAACTCTGAGC	1974
Db	1367	ACCAATATCTCTTCTTAGTGTAGCGGTATAGGCACCACTTCAAGAACTCTGAGC	1426
QY	1975	ACCGCTTACATACCTCGCTCTGCTAATCTGTTAACCATGSGCTGCTGCCAGTGCATTA	2034
Db	1427	ACCGCTTACATACCTCGCTCTGCTAATCTGTTAACCATGSGCTGCTGCCAGTGCATTA	1486
QY	2035	GTCGTGCTTACCGGGTTGACATCAAGACATATGTTACCGGATTAAGCGCAGCGTCCGG	2094
Db	1487	GTCGTGCTTACCGGGTTGACATCAAGACATATGTTACCGGATTAAGCGCAGCGTCCGG	1546
QY	2095	CTGAACCGGGGTTCTGTGCACACAGCCAGCTTSGAGCCAAAGACCTTACCCGATCTGAG	2154
Db	1547	CTGAACCGGGGTTCTGTGCACACAGCCAGCTTSGAGCCAAAGACCTTACCCGATCTGAG	1606
QY	2155	ATTACCTACAGCGTAGCTATGAGAAACCGCACGCTTCCCGAAGGGAAGAGCGCAG	2214
Db	1607	ATTACCTACAGCGTAGCTATGAGAAACCGCACGCTTCCCGAAGGGAAGAGCGCAG	1666
QY	2215	GTAATCCGTATACCGCAGGTCCGAACAGAGAGCGACAGAGGAGGCTTCCAGGGGGAAA	2274
Db	1667	GTAATCCGTATACCGCAGGTCCGAACAGAGAGCGACAGAGGAGGCTTCCAGGGGGAAA	1726

RESULT 7					
AX776824					
LOCUS	AX776824	5488 bp	DNA	linear	PAT 14-JUL-2003
DEFINITION	Sequence 6 from Patent WO03004055.				
ACCESSION	AX776824				
VERSION	AX776824.1				
KEYWORDS	GI:32694266				
ORGANISM	unidentified				
SOURCE	unidentified				
REFERENCE	unclassified.				
AUTHORS	1				
TITLE	Haynes, J.R. and Arrington, J.E.				
JOURNAL	Nucleic acid adjuvants				
	Patent: WO 03004055-A 6 16-JAN-2003;				
	Powderject Vaccines, Inc. (US)				
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DB	1067	AGACCAAGTTTAA	CTCATATATATCTTTAGATTGATTTAAACCTCATTTTATAATTAAAG	1126	1126
QY	1675	GATCAGGAGTGA	ATCTTTTGGATTAATCTCATGACCAAAATCCCTTAACGAGTTTC	1734	1734
DB	1127	GATCAGGAGTGA	ATCTTTTGGATTAATCTCATGACCAAAATCCCTTAACGAGTTTC	1186	1186
QY	1735	GTTCCACGTGAG	CGCAGCCCGGTGAAAAGATCAAGAATCTTCTAGATCCCTTTT	1794	1794
DB	1187	GTTCCACGTGAG	CGCAGCCCGGTGAAAAGATCAAGAATCTTCTAGATCCCTTTT	1246	1246

[illegible]

Db	3405	GTATTATTAACATAGCGTGAGATCTCACGCCAATCTCGGTAACGTTTCCGACATG	3464
Oy	3977	GGCTTTTCCGGTAGCGGCGAGCTTTCACATCCGAGCCCTGGTCCATGCTCCACGC	4036
Db	3465	GGCTTTTCCGGTAGCGGCGGAGCTTTCACATCCGAGCCCTGGTCCATGCTCCACGC	3524
Oy	4037	GCTCATGTCGCTCGGCACTCTTGTCTCTTAACAGTGGAGGCCAGACTTAAGCAACGA	4096
Db	3525	GCTCATGTCGCTCGGCACTCTTGTCTCTTAACAGTGGAGGCCAGACTTAAGCAACGA	3584
Oy	4097	CAATGCCACCAACCAACGATGTCGCGCAAGGCGCGGTGAGGATATGTCGTGAAA	4156
Db	3585	CAATGCCACCAACCAACGATGTCGCGCAAGGCGCGGTGAGGATATGTCGTGAAA	3644
Oy	4157	ATGAGCTTCGAGATTGGGCTCGCACCGCTGACGCGAGATGAAGAATTAAAGCAGCGCAG	4216
Db	3645	ATGAGCTTCGAGATTGGGCTCGCACCG-TGAAGCAGATGGAAGACTTAAGGCAAGCGAG	3703
Oy	4217	AAGAAGATGCAGGCGAGCTGAAGTTGTTGTAATCTGATTAAGACTCAGAGGTAATCCCGTTG	4276
Db	3704	AAGAAGATGCAGGCGAGCTGAAGTTGTTGTAATCTGATTAAGACTCAGAGGTAATCCCGTTG	3763
Oy	4277	CGGTCGCTTAACCGGTGAGGGCGAGTGAAGCTGACGAGTACTGTCGTCGCGCGCGG	4336
Db	3764	CGGTCGCTTAACCGGTGAGGGCGAGTGAAGCTGACGAGTACTGTCGTCGCGCGCGG	3823
Oy	4337	CCACCAGACATTAATAGCTGACAGACTTAACAGACTGTTCTTTCCATGGGTCTTTTCTGCA	4396
Db	3824	CCACCAGACATTAATAGCTGACAGACTTAACAGACTGTTCTTTCCATGGGTCTTTTCTGCA	3883
Oy	4397	GTCACCGTCCACGGCT 4412	
Db	3884	GTCACCGTCCACGGCT 3899	

Db	1187	GTTCACGTGAGCGCTACAGACCCCGGTAAGAAAAGATCAAAAGATCTTCTTGAGATCCTTTT	1246
Qy	1795	TCCTGCGGCTATCTGCTGCTTGCACAAACAAAAACACCGGCTACAGCGGTGGTTGTT	1854
Db	1247	TCTCGCGGTATCTGTGCTTGCACAAACAAAAACACCGGCTACAGCGGTGGTTGTT	1306
Qy	1855	GCCGGAATCAAGAGTACCAACTTTTTCGGAAGGTAACTGGCTTACAGAGGCGAGAT	1914
Db	1307	GCCGGAATCAAGAGTACCAACTTTTTCGGAAGGTAACTGGCTTACAGAGGCGAGAT	1366
Qy	1915	ACCAATACTGTTCTTCTAGTGTAAGCGGTAGTTAGGCACACACTTCAAGAACTCTGATG	1974
Db	1367	ACCAATACTGTTCTTCTAGTGTAAGCGGTAGTTAGGCACACACTTCAAGAACTCTGATG	1426
Qy	1975	ACCGCTTACATACCTCGCTCTGCTAATCTGTTAACCAATGGCTGCTGCAGTGGCGATTA	2034
Db	1427	ACCGCTTACATACCTCGCTCTGCTAATCTGTTAACCAATGGCTGCTGCAGTGGCGATTA	1486
Qy	2035	GTGCTGTCTTAACCGGGTGTGACCTCAACACGATATCTAACCGGATTAAGGCGAGCGGTGGG	2094
Db	1487	GTGCTGTCTTAACCGGGTGTGACCTCAACACGATATCTAACCGGATTAAGGCGAGCGGTGGG	1546
Qy	2095	CTGAACGGGGGTTCTGTGCACACAGCCAGCTTGAAGCGAACGACTTACACCGAATCTAG	2154
Db	1547	CTGAACGGGGGTTCTGTGCACACAGCCAGCTTGAAGCGAACGACTTACACCGAATCTAG	1606
Qy	2155	ATACCTTACAGCGTAGCTATGAGAAAGCGCACGCTTCCGAGGGAGAAAGGCTGACAG	2214
Db	1607	ATACCTTACAGCGTAGCTATGAGAAAGCGCACGCTTCCGAGGGAGAAAGGCTGACAG	1666
Qy	2215	GTATTCGGTAAACGGGACGGGTGCGAACAAGAGAGACGCAACGAGGGAGGCTTCCAGGGGGGAAA	2274
Db	1667	GTATTCGGTAAACGGGACGGGTGCGAACAAGAGAGACGCAACGAGGGAGGCTTCCAGGGGGGAAA	1726

LOCUS	AX776822	5500 bp	DNA	linear	PAT 14-JUL-2003
DEFINITION	Sequence 4 from Patent WO03004055.				
ACCESSION	AX776822				
VERSION	AX776822.1	GI:32694264			
KEYWORDS					
SOURCE	unidentified				
ORGANISM	unclassified				
REFERENCE	1				
AUTHORS	Haynes, J. R. and Arrington, J. E.				
TITLE	Nucleic acid adjuvants				
JOURNAL	Patent: WO 03004055-A 4 16-JAN-2003;				
FEATURES	Powderject Vaccines, Inc. (US)				
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	/note="DPJV2004 plasmid"				
ORIGIN					

	Query Match	37.1%	Score 2378.8	DB 6	Length 5500
	Best Local Similarity	91.6%	Pred. No. 0		
	Matches 2598	Conservative	0	Mismatches 197	Indels 41
				Gaps	6
QY	1615	AGCCTCAGGTACTATATATATCTTTAGATTGATTAAACCTCATTTTATTTAATAAAG	1674		
DB	1067	AGACCAAGTTTACTATATATATCTTTAGATTGATTAAACCTCATTTTATTTAATAAAG	1126		
QY	1675	GATCTAGGTGAAGATCTCTTTTGATATATCTCATGACCAAAATCCCTTAACGTGAGTTTC	1734		
DB	1127	GATCTAGGTGAAGATCTCTTTTGATATATCTCATGACCAAAATCCCTTAACGTGAGTTTC	1186		
QY	1735	GTTCACTGAGGCTCAGACCCCGTGAAAGATCAAGGATCTTCTTGAGATCCCTTTT	1794		

Db	1727	CGCCTGGATCTTTATATAGTCTCTGTGCGGGTTTCGCACTCTGACCTTAGAGGCTGCATTTTTT	1786
Qy	2335	GTGATGCTCGTCAGGGGGGGGGAGCCCTATGAGAAAAAGCCAGCAACGGCGCTTTTTCACG	2394
Db	1787	GTGATGCTCGTCAGGGGGGGGGAGCCCTATGAGAAAAAGCCAGCAACGGCGCTTTTTCACG	1846
Qy	2395	GTCCTGGCCCTTTTGCTGCGCCCTTTTGTGCACATGTCCTTTCCTGCGTATTCCTCGTATTC	2454
Db	1847	GTCCTGGCCCTTTTGCTGCGCCCTTTTGTGCACATGTCCTTTCCTGCGTATTCCTCGTATTC	1906
Qy	2455	TGTGGATTAACCGTATTAACCGCCATGACATTAAGTATTAATGATATC-----AATTA	2505
Db	1907	TGTGGATTAACCGTATTAACCGCTTTGATGATGACGTGATACCGCTGCGCGAGCGAAGAC	1966
Qy	2506	CGGGGTCATTAATTCATAGCCCATATATATGAGTTCCGCGTTACATPAACCTTAGGTTAATG	2565
Db	1967	CGAGCGCAGCAGATCAGTAGAGCCGAGGAAGCGGAAGAGCCCAATATAGCAAAACCGCTCT	2026
Qy	2566	GCCCGCCTGCGTGACCGCCCAACAGACCCCGCCCATTAGCCTCAATATAGACGAG-----	2620
Db	2027	CCCCGCGGTTGGCCGATTCATTAATGACAGCTGSCACGAGGTTTCCCGACTGGAAGC	2086
Qy	2621	-----ATGCAATTAAGTGACAGACGATATGAGGCTATATCG	2657
Db	2087	GGGCAGTAGCGGCAACGCATTAATATGATGATGACTCACTCATTTAGGCAACCCAGCGCTTT	2146
Qy	2658	CCGATAGAGCGGACATCAAGCTGSCACATGCGCAATGCAATATGATCTATATCATTTGAAATC	2717
Db	2147	ACACTTATATGCTTCGCGGCTCGTAGTGTTGTGTGGAATTTGTGAGCGGATTAACATTTTCAC	2206
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RESULT 10
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 ACCESSION AF430344
 VERSION AF430344.1 GI:16798502
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct
 artificial sequences.
 REFERENCE
 1 (bases 1 to 9918)
 Smith,J.M., Ellenberger,D., Heneline,W., Campbell,D., Yi,H.,
 Folks,T.M., and Robinson,H.L.
 Multiprotein-expressing DNA Component for a DNA/MVA Vaccine for
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 TITLE
 Unpublished
 JOURNAL
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 Smith,J.M., and Robinson,H.L.
 AUTHORS
 Direct Submission
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 Submitted (09-OCT-2001) Microbiology and Immunology, Yerkes
 Regional Primate Research Center, 954 Gatewood RD NE, Atlanta, GA
 30329, USA
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527 CGTCCCGTCAAGTCAAGGCTATGCTCTGCAAGTTTCAACCAATTAACCAATTTGATT 586
1802 CGTCCCGTCAAGTCAAGGCTATGCTCTGCAAGTTTCAACCAATTAACCAATTTGATT 1861
587 AGAAAACTCATGAGCATCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 646
1862 AGAAAACTCATGAGCATCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 1921
647 CATATTTTGAAGAGCGTTTCTGTATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 706
1922 CATATTTTGAAGAGCGTTTCTGTATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1981
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2222 CTTGAGCGAGACGAATTAACGAGATGCTGTTTAAAGCAATTAACCAAGCAATGCAAT 2281
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2798 ----- 2797
1667 TTTAAAGAGTCAAG 1726
2829 CATGAGCGGATCATATTTGAATGATTTAGAAA-----ATTAACCAATGAGGCTTCCG 2884
1727 GAGTTTTCGTTCCACTGAGGCTGACCCCGTAGAAAAGATCAAGAGATCTTTGAGAT 1786
2885 GCACTT----- 2891
1787 CTTTCTTTTCTGCGGCTATCTGCTCTGCTGCAAAACAAACCAACCGCTACAGAGGCTG 1846
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2936 ----- 2935
1907 GCGCAGATACCAATATCTGTTCTTATGATGACCGTATAGGCAACCACTTCAAGAAC 1966
2936 ----- 2935
1967 TCTGTAGCACCGCTTACATACCTGCTGCTGTAATCTGTTTACCAAGTGTGCTGCCAGT 2026
2936 -----TGAATTAACCTTATTAATAAATAAGGGTATCAACGAG 2969
2027 GCGGATTAAGTGTGCTTACCGGGTTGACTCAAGAGATGATTAACCGGATTAAGGGCAG 2086
2970 GCGGATTAAGTGTGCTTACCGGGTTGACTCAAGAGATGATTAACCGGATTAAGGGCAG 2982
2087 CCGTCCGGCTGAACGGGGGCTGTCACACACCGCAGTTGAGAGCAACGACTTACACC 2146
2983 ----- 2982
2147 GAACTGATATCTTACAGCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2206
2983 -----CGCGCTTTTGGTGTATGACGATGAAAACCTCTGACACATGACAGCTTCCGGAGAC 3036
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3096 CGGG----- 3099

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Db 3100 ----- 3099
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Db 3100 ----- 3099
QY 2447 CCTGATTTCTGTGATAACGATATTACCGCATGATTAATTAAATGATCAATTAC 2506
Db 3100 ----- 3099
QY 2507 GGGGTCATTAGTTCATAGCCCATATATGAGTTCGCGTTACATACTTACGGTAAATG 2566
Db 3100 -----TGTGGCGGGTGT 3112
QY 2567 CCCGCTGGCTGACCGGCCAACGACCCCGCCATTGAGCTCAATAATGACGATCTGA 2626
Db 3113 CGGGGCTGGCTTAACTATGCGGATCAAGACAGATGTACTGAGAGTGCACCATATGCGG 3172
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Db 3173 TGTGAATACCGACAGATGCG----- 3194
QY 2687 GGGCAATGCAATTCATATACATTTGAATCAATTAATTGGCAATTAAGCATATTAATCATT 2746
Db 3195 -----T 3195
QY 2747 GGTATATAGCATTAATCAATTTGGCTATTGGCCATTGCAATAGTTTATCTATATCAT 2806
Db 3196 AAGAGAAATTAACCGCATCGATGCTATTTGGCCATTGACATAGCTGATTCATATCAT 3255
QY 2807 AATATGACATTTATTTGCTCATGTCCAAATATGACCGCCATGTTGACATTTGATTTG 2866
Db 3256 AATATGACATTTATTTGCTCATGTCCAAATATGACCGCCATGTTGACATTTGATTTG 3315
QY 2867 ACTAGTTATTAATAGTAAATCAATTAACGGGCTCATTTAGTTATAGCCCATATATGAGTTC 2926
Db 3316 ACTAGTTATTAATAGTAAATCAATTAACGGGCTCATTTAGTTATAGCCCATATATGAGTTC 3375
QY 2927 CGGTTATCATTAACCTTAAGGTAATGCGCGCTGCTGACCGCCCAACGACCGCCGCCA 2986
Db 3376 CGGTTATCATTAACCTTAAGGTAATGCGCGCTGCTGACCGCCCAACGACCGCCGCCA 3435
QY 2987 TTGACGTCATTAAGTATGATGTTCCCATAGTAAACGCAATTAAGGACCTTTCATTTGACGT 3046
Db 3436 TTGACGTCATTAAGTATGATGTTCCCATAGTAAACGCAATTAAGGACCTTTCATTTGACGT 3495
QY 3047 CAATGGGTGAGTATTTTACGGTAAACCTGGCACTTGGCAGTACATCAAGTATCATATG 3106
Db 3496 CAATGGGTGAGTATTTTACGGTAAACCTGGCACTTGGCAGTACATCAAGTATCATATG 3555
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QY 3287 GGAATTTCAAAGTCTCCACCCCATTTGACGTCATAGGAGTTTGTGTTGGCACCAAATCAA 3346
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QY 3407 GTACGGTGGAGGTCTATATAGCAGAGCTGTTTATGAAACCGTCAGATCGCTGGAGA 3466

Db 3856 GTACGGTGGAGGTCTATATTAAGCAGAGCTCGTTAGTGAACCGTCAGATCGCTGGAGA 3915
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QY 3527 CGGAAACGCTGATTTGAAACGCGGATTTCCCGTGGCAAGAGTGAAGTAAAGTACCGCTAT 3586
Db 3976 CGGAAACGCTGATTTGAAACGCGGATTTCCCGTGGCAAGAGTGAAGTAAAGTACCGCTAT 4035
QY 3587 AGACTCTATAGGACACACCCCTTGGCTTATGATGATGCTATACCTGTTTGGCTGGGC 3646
Db 4036 AGACTCTATAGGACACACCCCTTGGCTTATGATGATGCTATACCTGTTTGGCTGGGC 4095
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QY 3947 CCGGAATCTGGGATGCTGTTCCGACATGCGCTCTTCTCGGATGCGCGGAGCTTCCA 4006
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QY 4007 CATCCGAGCCCTGCTGCTCCATGCTCCAGGCGCTCAAGTGGCTCGGACGCTCGTCTCC 4066
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Db 4576 AGGCGTGGCGGTAGGATGCTGTGAATAAGCTCGAAGTTGGCTCGCACCGCTG 4635
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Db 4696 TCTGATTAAGTACAGAGTAACTCCCGTGGCGGTGCTTTAAACGCTGAGGCGAGTGA 4755
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Db 4816 GACTGTTCTTTCCATGAGGCTTTTCTGAGTCAACCGTCCAG 4858

RESULT 13
BD000697 5108 bp DNA linear PART 31-JAN-2002
LOCUS BD000697
DEFINITION Growth hormone and growth hormone-releasing hormone composition.
ACCESSION BD000697

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RESULT 14
BD000698 5108 bp DNA linear PAT 31-JAN-2002
LOCUS BD000698
DEFINITION Growth hormone and growth hormone-releasing hormone composition.
ACCESSION BD000698.1 GI:18623811
VERSION JP 2000350590-A/51.
KEYWORDS JP 2000350590-A/51.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 5108)
Morsey, M.A. and George, M.
Growth hormone and growth hormone-releasing hormone composition
Patent: JP 2000350590-A 51 19-DEC-2000;
PRIZER PROD INC

COMMENT
OS Artificial Sequence
PN JP 2000350590-A/51
PD 19-DEC-2000
PR 12-APR-2000 JP 2000111120
PI MOHAMMED ALI MORSEY, MICHAEL GEORGE
PC C12N15/09, A01K67/027, A61K31/711, A61K38/27, A61K38/04, A61K48/00,
PC A61P5/02,
PC A61P43/00, C07K14/60, C12N5/10// (C12N5/10, C12R1:91), C12N15/00,
PC A61K37/36,
PC A61K37/43, C12N5/00, (C12N5/00, C12R1:91)
CC
FH
FT
FT source 1. 5108
Location/Qualifiers
1. 5108
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 31.3%; Score 2008.6; DB 6; Length 5108;
Best Local Similarity 74.2%; Pred. No. 0;
Matches 3058; Conservative 0; Mismatches 239; Indels 826; Gaps 8;

QY 467 GGAAGATGGGTGATCTGATCTTCAACTGACGAAAGTTGATTTATGACGAAGCGC 526
DB 1742 GGAAGATGGGTGATCTGATCTTCAACTGACGAAAGTTGATTTATGACGAAGCGC 1801
QY 527 CGTCCGCTCAAGTCAAGTAACTGCTGCGAGTGTACCAACAAATTAACCAATTCGATT 586
DB 1802 CGTCCGCTCAAGTCAAGTAACTGCTGCGAGTGTACCAACAAATTAACCAATTCGATT 1861
QY 587 AGAAAACTCATGACATCAATTAATGAATGCAATTTATCATATGAGATTATCAATAC 646
DB 1862 AGAAAACTCATGACATCAATTAATGAATGCAATTTATCATATGAGATTATCAATAC 1921
QY 647 CATATTTTGAAGAAACCGTTTCTGTATGAAGAGAGAGAAATCAACGAGGCACTTCATA 706
DB 1922 CATATTTTGAAGAAACCGTTTCTGTATGAAGAGAGAGAAATCAACGAGGCACTTCATA 1981
QY 707 GGATGGCAAGATCTGATATCGGTGCGATTGCGACTGCTGCAATCAATCAATCAACTTA 766
DB 1982 GGATGGCAAGATCTGATATCGGTGCGATTGCGACTGCTGCAATCAATCAATCAACTTA 2041
QY 767 TTAATTTCCCTGCTGCAAAATTAAGTTATCAAGTGAAGAAATCAATGATGACGACTG 826
DB 2042 TTAATTTCCCTGCTGCAAAATTAAGTTATCAAGTGAAGAAATCAATGATGACGACTG 2101
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DB 2102 AATCCGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2161
QY 887 CATTAAGCTGCTGATCAAAATCACTGCAATCAACCAACCGTATTCATCGTATTCG 946
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RESULT 15

AX138936

LOCUS AX138936 5111 bp DNA linear PAT 30-MAY-2001

DEFINITION Sequence 55 from Patent EP1052286.

ACCESSION AX138936

VERSION AX138936.1 GI:14274641

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Morsey, M.A. and Sheppard, M.G.

TITLE Growth hormone and growth hormone releasing hormone compositions

JOURNAL Patent: EP 1052286-A 55 15-NOV-2000;

Pflizer Products Inc. (US)

Location/Qualifiers

FEATURES

source

1. 5111

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="pGHRH-291a1a1522CMV construct"

ORIGIN

Query Match 31.3%; Score 2008.6; DB 6; Length 5111;
Best Local Similarity 74.2%; Pred. No. 0;
Matches 3059; Conservative 0; Mismatches 239; Indels 826; Gaps 8;

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Qy 347 TGAATCGCCCATCATCCAGCCAGAAAGTGAAGGAGCCAGTGTGAAGAGCTTTGTT 406
Db 1622 TGAATCGCCCATCATCCAGCCAGAAAGTGAAGGAGCCAGTGTGAAGAGCTTTGTT 1681
Qy 407 TAGGTGACCAAGTTGGTATTTTGAACCTTTTGTCCAGCGAAGGTCTGGTTGTCG 466
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Job time : 24056 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2004, 14:01:32 ; Search time 14701 Seconds
(without alignments)
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Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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VERSION AK014619.1 GI:128652585
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3

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QY 5949 CTTTGGGCGGCGATGATGAGGGGCGTCTCTCACTGCTGCGAGGGCTTGTAGCTT 6008

Db 1535 TCTTGGGCGGCGATGATGAGGGGCGTCTTATGCTGAGCTCTCTGGGCTTACAGATAG 1594

QY 6009 GCTGTGTCTGTC-----ACAAAGAGAGCAAGCTTCTTAAGAAAAGCAAGCACTCT 6059

Db 1595 GCTATGCTCTTCAAG 1654

QY 6060 CATGAG 6116

Db 1655 CATGAG 1714

QY 6117 AATAGAGTGGGCGCAAAAGGCTGACCTCACTTACT 6154

Db 1715 AACAGAGTGGGCGCAAAAGGCTTATCACTCACTGACCT 1752

RESULT 2
BM463960 1063 bp mRNA linear EST 05-FEB-2002
LOCUS BM463960 AGENCOURT 6445513 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5539977
DEFINITION 5', mRNA sequence.
ACCESSION BM463960

VERSION BM463960.1 GI:18513002
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1063)
NIH-MGC <http://mgs.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE Email: cgabs-remail.nih.gov
COMMENT Tissue Procurement: ARCC/DCTP/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Plate: LLM12235 row: f column: 10
High quality sequence stop: 749.

FEATURES
source
1. 1063
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5539977"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

ORIGIN
Query Match 13.8%; Score 885.8; DB 12; Length 1063;
Best Local Similarity 96.1%; Pred. No. 36-243; Indels 5; Gaps 3;
Matches 937; Conservative 0; Mismatches 33;

QY 4497 TGGTGAATTCGAGGAAGATGCTCGGCTGTTTGTACTGCTGCTGAGTTTCA 4556

Db 94 TGGAGAGCTAGAGAGAAATGCTCTGCGCTGTTTGTACTGCTGCTGAGTTTCA 153

QY 4557 GACCTCGGCGCATTTCCCTAGAGGCTGTGTCTCTTAAGAACTGATGAGAGGA 4616

Db 154 GACCTCGGCGCATTTCCCTAGAGGCTGTGTCTCTTAAGAACTGATGAGAGGA 213

QY 4617 ATGCTGTCAACCGTGAAGCGGGAGAGAGATCCCTGTGGCAAGTTTCAGGAGAGTTTC 4676

Db 214 ATGCTGTCAACCGTGAAGCGGGAGAGAGATCCCTGTGGCAAGTTTCAGGAGAGTTTC 273

QY 4677 CTGTCAAGATATCCTTGTGCAATGACACCACTTGGGCTCAATTTCCCTTCAAGAGGAT 4736

Db 274 CTGTCAAGATATCCTTGTGCAATGACACCACTTGGGCTCAATTTCCCTTCAAGAGGAT 333

QY 4737 GGATGACCGGAGAGTGTGAGGCTTCCGCTTTTATATAGAACCTGCCAGTGTGCAAA 4796

Db 334 GGATGACCGGAGAGTGTGAGGCTTCCGCTTTTATATAGAACCTGCCAGTGTGCAAA 393

QY 4797 CTTTATGAGATTAACCTGTGGAACCTGCAAGTTTGGCTTTTGGGAGCAAACTGCAAGA 4856

Db 394 CTTTATGAGATTAACCTGTGGAACCTGCAAGTTTGGCTTTTGGGAGCAAACTGCAAGA 453

QY 4857 GAGACGACTCTGGTGAAGAGAAACATCTTGATTTGAGTGCCCAAGAGAGCAAAAT 4916

Db 454 GAGACGACTCTGGTGAAGAGAAACATCTTGATTTGAGTGCCCAAGAGAGCAAAAT 513

QY 4917 TTTTGCTTACTCTTATTAAGAAAGCATATCACTGATATGATATCCCATAGG 4976

Db 514 TTTTGCTTACTCTTATTAAGAAAGCATATCACTGATATGATATCCCATAGG 573

QY 4977 GACCTATGGCAATGAAATGATGATCAACCACTTTTAAGCAATCATATATTATGA 5036

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Db      574 GACCTATGCCCAATGAAAATGATCAACCCCATGTTTAAAGACATCAATATTATGA 633
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      634 CCTCTTTGTGTGATGATTAATATGTCATTAAGATGACCTGTTGGGGATCTGAAAT 693
      5097 CTGAGAGACATTGATTTTCCCATGAGACACGCTTTCTGCTTGGCATGACTCTT 5156
      694 CTGAGAGACATTGATTTTCCCATGAGACACGCTTTCTGCTTGGCATGACTCTT 753
      5157 CTTGTGGCGGTGGGAACAAGATCCAGAACTGACAGAGATGAAAACTTCACTATTC 5216
      754 CTTGTGGCGGTGGGAACAAGATCCAGAACTGACAGAGATGAAAACTTCACTATTC 813
      5217 ATATTGGAGACTGGCGGATGACAGAAAGTGTGACATTGGACAGATAGATGATGGAGG 5276
      814 ATATTGGAGACTGGCGGATGACAGAAAGTGTGACATTGGACAGATAGATGATGGAGG 873
      5277 TCAGACACCCCAAAATCTTAATCTCTCAGCCGACATCTTCTCTCTTGGCAGAT 5336
      874 TCAGACACCCCAAAATCTTAATCTCTCAGCCGACATCTTCTCTCTTGGCAGAT 932
      5337 TGTCTGTAGCCGATTTGAGAGAGTCAACAGCCATCACTTTTATGCAATGGAACGCCGA 5396
      933 TGTCTGTAGCCGATTTGAGAGAGTCAACAGCCATCACTTTTATGCAATGGAACGCCGA 992
      5397 GGAACCTTTACGGGTATCTCTGGAACCATGACAAATCCAGAACCCCAAGCTCCCTC 5456
      993 GGAACCTTTACGGGTATCTCTGGAACCATGACAAATCCAGAACCCCAAGCTCCCTC 1048
      5457 TTCAGTGATGTAGA 5471
      1049 TTCANCTAAGTANA 1063

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RESULT 3
LOCUS   BU190117                      984 bp    mRNA    linear    EST 04-SEP-2002
DEFINITION  AGENCOURT_8076683 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089012
ACCESSION  BU190117
VERSION    BU190117.1 GI:22704101
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 984)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
AUTHORS    Contact: Robert Strausberg, Ph.D.
            Email: cgabs-remail.nih.gov
            Tissue Procurement: DCTD/DRP
            CDNA Library Preparation: Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: LNCM2328 row: b column: 21
            High quality sequence stop: 661.
FEATURES
            Location/Qualifiers
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                /organism="Homo sapiens"
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                /db_xref="taxon:9606"
                /clone="IMAGE:6089012"
                /issue_type="melanotic melanoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /clone_id="NIH_MGC_112"
                /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:

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Ecoli; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

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ORIGIN
Query Match      13 6%; Score 874.6; DB 13; Length 984;
Best Local Similarity 96.8%; Pred. No. 4,8e-240;
Matches 926; Conservative 0; Mismatches 29; Indels 4; Gaps 3;

      4510 GGAAGAAATCTCTCGCTGCTTTTGTACTGCTCTGCTGAGATTCACAGCTCCGCTGAC 4569
      4 GGAAGAAATCTCTCGCTGCTTTTGTACTGCTCTGCTGAGATTCACAGCTCCGCTGAC 63
      4570 CATTTCCCTAGAGCTGTGTCTCTCTTAAGAACCTGATGAGAGAAATGCTGCCACCG 4629
      64 CATTTCCCTAGAGCTGTGTCTCTCTTAAGAACCTGATGAGAGAAATGCTGCCACCG 123
      4630 TGAAGGGGGAGACAGAGATCCGTGAGCAGCTTTGAGAGAGATTCCTGTGAGATATTC 4689
      124 TGAAGGGGGAGACAGAGATCCGTGAGCAGCTTTGAGAGAGATTCCTGTGAGATATTC 183
      4690 CTTCTGTCCAAATGACACCACTTGGGCTCAATTTCCCTTACAGAGGGTGTGATGACGGGAG 4749
      184 CTTCTGTCCAAATGACACCACTTGGGCTCAATTTCCCTTACAGAGGGTGTGATGACGGGAG 243
      4750 TCGTGACCTTCCTGCTTTTATTAATAGACCTGCACTGCTCTGGCAATCTTCATGGATTC 4809
      244 TCGTGACCTTCCTGCTTTTATTAATAGACCTGCACTGCTCTGGCAATCTTCATGGATTC 303
      4810 AACTGTGAGAAACCTGCAAGTTTGGCTTTGGGGACCAAACTGCAAGAGAGACGACTTGG 4869
      304 AACTGTGAGAAACCTGCAAGTTTGGCTTTGGGGACCAAACTGCAAGAGAGACGACTTGG 363
      4870 GTGAGAGAAACATCTTCAATTTGATGATGAGCCCGCAGAGAGACAAATTTTGGCTACTTC 4929
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      4930 ACTTTAGCAAGACATACATCACTGATGATGATGATGATGATGATGATGATGATGATGATG 4989
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      4990 ATGAAAAATGAGATCAACCCCATGTTTAAGACATATTTATGATGATGATGATGATGATGATG 5049
      484 ATGAAAAATGAGATCAACCCCATGTTTAAGACATATTTATGATGATGATGATGATGATGATG 543
      5050 ATGCAATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5109
      544 ATGCAATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 603
      5110 GATTTTGGCCCATGAGACACAGCTTTTGGCTTGGCATAGACTCTTCTTGGCGGTGG 5169
      604 GATTTTGGCCCATGAGACACAGCTTTTGGCTTGGCATAGACTCTTCTTGGCGGTGG 663
      5170 GAACAAAGAAATCCAGAGCTGACAGAGATGAAAACTTCACTATTCATTTGGGACTGG 5229
      664 GAACAAAGAAATCCAGAGCTGACAGAGATGAAAACTTCACTATTCATTTGGGACTGG 723
      5230 CGGATGACAGAAAGTGTGACATTTGACAGATGATGATGATGATGATGATGATGATGATGATG 5289
      724 CGGATGACAGAAAGTGTGACATTTGACAGATGATGATGATGATGATGATGATGATGATGATG 783
      5290 AATCTTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5349
      784 AATCTTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 843
      5350 -TTGAGAGATTAACAAGCATATGCTTTTATGCAATGG--AACGCCAGAGGACCTTTA 5406
      844 TTGAGAGATTAACAAGCATATGCTTTTATGCAATGGAAAGCCCGAGGGGACCTTTA 903

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location/Qualifiers
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/clone="IMAGE:5547850"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."

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Db	45	TGTGAGCACTAGAGGAAGAATGCTCTGGCTGTTTTGTATAGTCCGTGCTGGAGTTTCCA	104
QY	4557	GACCTCCGCTGGCCATTTTCCTAGAGCCTGTGTCTTCTCTTAAGAACTGATGAGAGAAGA	4618
Db	105	GACCTCCGCTGGCCATTTTCCTAGAGCCTGTGTCTCTCTTAAGAACTGATGAGAGAAGA	164
QY	4617	ATGCTGTCCACCGTGGAGCGGGGACAGGAGTCCCTGTGGCCAGCTTTACAGGCAGAGTTC	4676
Db	165	ATGCTGTCCACCGTGGAGCGGGGACAGGAGTCCCTGTGGCCAGCTTTACAGGCAGAGTTC	224
QY	4677	CTGTGAGAAATATCTTTCTGTCCAAATGCACCACTTGGGCTCAATTTCCCTTTCACAGGGGT	4738
Db	225	CTGTGAGAAATATCTTTCTGTCCAAATGCACCACTTGGGCTCAATTTCCCTTTCACAGGGGT	284
QY	4737	GGATGACCGGAGTGCTGGCCCTTCGTCTTTTATATATAGAACTTGCCAGTGTCTGGGCAA	4798
Db	285	GGATGACCGGAGTGCTGGCCCTTCGTCTTTTATATATAGAACTTGCCAGTGTCTGGGCAA	344
QY	4797	CTTCATGGGATTTCAACTGTGGAATCTGCAAGTTTGGCTTTTGGGACCAAACTGCACAGA	4855

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RESULT 5
LOCUS      BU183039
DEFINITION
ACCESSION  BU183039
VERSION    BU183039
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE      1 (bases 1 to 903)
JOURNAL    NIH-MGC http://mgc.nci.nih.gov/.
COMMENT    National Institutes of Health, Mammalian Gene Collection (MGC)
           Unpublished (1999)
           Contact: Robert Strausberg, Ph.D.
           Email: CGAPds-remail.nih.gov
           Tissue Procurement: ATCC/DCTP/DMP
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
           DNA Sequencing by: Agencourt Bioscience Corporation

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM13502 row: 1 column: 07
High quality sequence stop: 683.
Location/Qualifiers

FEATURES

source

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1. 903
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
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/note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."
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ORIGIN

Query Match

13.1%; Score 837; DB 13; Length 903;

Best Local Similarity 97.6%; Pred. No. 3.3e-229;

Matches 880; Conservative 0; Mismatches 18; Indels 4; Gaps 3;

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QY 4552 TTCGAGCCTCGCGTCCATTTCCCTAGAGCCTGTGTCTCTTAAGAACTGATGAG 4611
DB 1 TTCGAGACCTCCGCTGGCCATTTCCCTAGAGCCTGTGTCTCTTAAGAACTGATGAG 60
QY 4612 AAGGATGCTGTCCACCGTGGAGCGGGGACAGAGTCCCTGTCGCGACCTTACGACAG 4671
DB 61 AAGGATGCTGTCCACCGTGGAGCGGGGACAGAGTCCCTGTCGCGACCTTACGACAG 120
QY 4672 GGTTCCTGTCAGATATCTCTTGTGTCATGACCACTTGGGCTCAATTTCCCTTACA 4731
DB 121 GGTTCCTGTCAGATATCTCTTGTGTCATGACCACTTGGGCTCAATTTCCCTTACA 180
QY 4732 GGGGTGATGACCGGGAGTGTGAGCTTCCGCTTTTAATAGACCTGCAGTGTCT 4791
DB 181 GGGGTGATGACCGGGAGTGTGAGCTTCCGCTTTTAATAGACCTGCAGTGTCT 240
QY 4792 GGAACCTTCATGGGATTCATCTGTGAAATGCAAGTTGGCTTTGGGACCAATGTC 4851
DB 241 GGAACCTTCATGGGATTCATCTGTGAAATGCAAGTTGGCTTTGGGACCAATGTC 300
QY 4852 ACAGAGAGACGACTCTTGTGAGAAAGAAATCATCTTGCATTTGAGTGTGATCC 4911
DB 301 ACAGAGAGACGACTCTTGTGAGAAAGAAATCATCTTGCATTTGAGTGTGATCC 360
QY 4912 AAATTTTGTGCTACCTGACTTGTAGCAAGACATACATGCTCAGACTATGTCTCC 4971
DB 361 AAATTTTGTGCTACCTGACTTGTAGCAAGACATACATGCTCAGACTATGTCTCC 420
QY 4972 ATAGGAGACCTATGAGCCAAATGAAATGATTCAAACCCATGTTTAAACGACATAT 5031
DB 421 ATAGGAGACCTATGAGCCAAATGAAATGATTCAAACCCATGTTTAAACGACATAT 480
QY 5032 TATGACCTCTTGTGATGATGATTTATATGTGTCAATGATGATGATGATGATGAT 5091
DB 481 TATGACCTCTTGTGATGATGATTTATATGTGTCAATGATGATGATGATGATGAT 540
QY 5092 GAAATCTGAGAGACATGATTTTGTCCATGAAACACAGCTTTCGCTTGGCATAGA 5151
DB 541 GAAATCTGAGAGACATGATTTTGTCCATGAAACACAGCTTTCGCTTGGCATAGA 600
QY 5152 CTCTTCTTGTGGGTGGGAAACAAGAAATCCAGAAGCTGACAGAGATGAAATCTTCA 5211
DB 601 CTCTTCTTGTGGGTGGGAAACAAGAAATCCAGAAGCTGACAGAGATGAAATCTTCA 660
QY 5212 ATTCCATATTTGGGAGTGGGGAGTGCAGAAAGTGTGACATTTGCAAGATGATGATGAT 5271
DB 661 ATTCCATATTTGGGAGTGGGGAGTGCAGAAAGTGTGACATTTGCAAGATGATGATGAT 720
QY 5272 G-GAGGTGACAGCCCAAAATCTTAATTACTAGCCGACATCTTCTCTCTTG 5330
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DB 721 GAGAGTGCAGACCCCAAAATCTTAATTACTAGCCGACATATCTTCTCTCTTG 780

QY 5331 GCAGATTTGCTGTAGGCG-CATTGAGAGATGACAAAGCCATCATGCTTTATGCAATGGA 5389

DB 781 GCAGATTTGCTGTAGGCGATTTGAGAGTACCAAGCCATCATGCTTTATGCAATGGA 840

QY 5390 CCGCCGAGGGA--CCTTACGGCGTATCTGTAACCAATGCAAAATCCAGAACCCGAG 5447

DB 841 ACGCCGAGNACCTTTACNCGGTATCTGTAATCTGAAACCATGACAAATCAGAACCCGAG 900

QY 5448 GC 5449

DB 901 GC 902

RESULT 6

B0682227 866 bp mRNA linear EST 15-JUL-2002

LOCUS AGENCOURT 8208342 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6262799

DEFINITION 5', mRNA sequence.

ACCESSION B0682227

VERSION B0682227.1 GI:21794906

KEYWORDS

EST.

SOURCE

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 866)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: DCTD/DRP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2425 row: k column: 24

High quality sequence stop: 661.

Location/Qualifiers

1. 866

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/mol_type="mRNA"

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/tissue_type="melanotic melanoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 112"

/note="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGAG(G). Library constructed by Ling Hong in the

Laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

ORIGIN

Query Match 12.9%; Score 829.4; DB 13; Length 866;

Best Local Similarity 98.4%; Pred. No. 5e-227;

Matches 847; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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DB 2 GAGGAAGATGCTCTGCGCTGTTTGTACTGCTGTGAGATTCAGACCTCGCTGG 61
QY 4569 CCATTTCCCTTAAGCCTGTGTCTCTCTTAAGAACTGATGAGAGAAATGCTGTCCACC 4628
DB 62 CCATTTCCCTTAAGCCTGTGTCTCTCTTAAGAACTGATGAGAGAAATGCTGTCCACC 121
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Qy 4629 GTGGAGGGGGGACAGAGTCCCTGTGGCCAGCTTTCAGGCGAGAGTTCCTGTGAGATAT 4688
Db 122 GTGGAGGGGGGACAGAGTCCCTGTGGCCAGCTTTCAGGCGAGAGTTCCTGTGAGATAT 181
Qy 4689 CCTTCTGTCCAAATGACACCACTTGGGCTCAATTTCCCTTCACAGGGGTGATGACCGGGA 4748
Db 182 CCTTCTGTCCAAATGACACCACTTGGGCTCAATTTCCCTTCACAGGGGTGATGACCGGGA 241
Qy 4749 GTCGTGCTTCCCTCTTTTATTAATAGACCTGCGAGCTCTGTGCAACTTCATGGGAT 4808
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Qy 4809 CAATGTGAAACCTGCAAGTTGGCTTTGGGACCAACCTGCAAGAGACGACCTT 4868
Db 302 CAATGTGAAACCTGCAAGTTGGCTTTGGGACCAACCTGCAAGAGACGACCTT 361
Qy 4869 GGTGAGAGAAACCTTTCATTTGAGTGGCCCCAGAGAGGACAAATTTTGGCTTACT 4928
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Qy 4929 CACTTTCAGAAAGCATACCATGCTGAGCTGATGTCATCCCATAGGAGCTATGGCA 4988
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Qy 5109 TGATTTTGGCCATGAGACACCAAGCTTTTCTGCTTGCATAGACTCTTCTTGTGCGGT 5168
Db 602 TGATTTTGGCCATGAGACACCAAGCTTTTCTGCTTGCATAGACTCTTCTTGTGCGGT 661
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Qy 5229 GCGGGATGCAAGAAAGTGTGACATTTGACAGATGATGATGATGATGATGATGATGATGAT 5288
Db 722 GCGGGATGCAAGAAAGTGTGACATTTGACAGATGATGATGATGATGATGATGATGATGAT 781
Qy 5289 AAATCTTAATCTGACGCGCAGATGATCTTCTCTTGGAGATGATGATGATGATGATGAT 5347
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Qy 5348 GATTGAGAGATGACACACCC 5368
Db 842 GATTGAGAGATGACACACCC 862

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RESULT 7
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DEFINITION AGENCOURT 8209637 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6272720
5', mRNA sequence.
ACCESSION B0677071
VERSION B0677071.1 GI:21789750
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 943)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@dbp-riemail.nih.gov
Tissue Procurement: DCTD/DTP

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/notes="Organ: skin; Vector: pOT87; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 12.9%; Score 828.4; DB 13; Length 943;
Best Local Similarity 97.7%; Pred. No. 1e-226;
Matches 881; Conservative 0; Mismatches 15; Indels 6; Gaps 4;

Qy 5089 TATGAAATCTGAGAGACATTTGATTTTGGCCATGAGACACAGCTTTTCTGCTTGGCAT 5148
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Qy 5149 AGACTCTTCTTGTGGGCTGAGAGAAATCCAGAGCTGACAGAGTGAATCTT 5208
Db 60 AGACTCTTCTTGTGGGCTGAGAGAAATCCAGAGCTGACAGAGTGAATCTT 119
Qy 5209 ACTATTCATATTTGAGACTGCGCGAGATGACAGAAAGTGTGACATTTGACAGATGATAC 5268
Db 120 ACTATTCATATTTGAGACTGCGCGAGATGACAGAAAGTGTGACATTTGACAGATGATAC 179
Qy 5269 ATGGAGGTGACACCCCAATCTTAATCTGACGCCAGCATCTTCTCTCT 5328
Db 180 ATGGAGGTGACACCCCAATCTTAATCTGACGCCAGCATCTTCTCTCT 239
Qy 5329 TGCGAGATGTCTGTAGCGGATTTGAGAGATGACAGACCATGATCTTATGCAATGGA 5388
Db 240 TGCGAGATGTCTGTAGCGGATTTGAGAGATGACAGACCATGATCTTATGCAATGGA 299
Qy 5389 ACGCCGAGGAGCTTTTACGCGCTAATCTGAGAAACATGACAAATCCAGAACCCCAAG 5448
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Qy 5509 ATGATTAAGCTGCGCAATTTACCTTGAATATCACTGGAAGATTTGTAGTCACTT 5568
Db 420 ATGATTAAGCTGCGCAATTTACCTTGAATATCACTGGAAGATTTGTAGTCACTT 479
Qy 5569 ACTGAGATAGCGGATCTCTCAAGACAGATGACATGCTTGGACATCTATATGATGAT 5628
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Qy 5629 GGAACATGTCCAGGATGACGAGATCTGCCACGATCTTCTTCTTCAACATGCA 5688
Db 540 GGAACATGTCCAGGATGACGAGATCTGCCACGATCTTCTTCTTCAACATGCA 599
Qy 5689 TTGTTGACAGATTTTGTGACAGTGGCTCCGAGAGCACCGTCTCTTCAAGAGTTAT 5748

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REFERENCE 1 (bases 1 to 908)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DRP
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: L1AM13511 row: b column: 03
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 /clone="IMAGE:6160418"
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 /lab_host="DH10B (phage-resistant)"
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 Best Local Similarity 96.1%; Pred. No. 1.3e-216;
 Matches 863; Conservative 0; Mismatches 21; Indels 7; Gaps 5;
 Db 4852 ACAGAGAGAGAGCTCTTGGTGAAGAAACCTTCGATTGAGTCCCGAGAGAGAC 4911
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 Qy 4912 AAAATTTTGGCTACCTTCACTTGAAGAAAGATACATGCTGAGCTATGTCATGCTCC 4971
 Db 60 AAAATTTTGGCTACCTTCACTTGAAGAAAGATACATGCTGAGCTATGTCATGCTCC 119
 Qy 4972 ATAGGAGACTATGAGCCAAATGAATGAATGATCAACCCATGTTTAAGCATCATATT 5031
 Db 120 ATAGGAGACTATGAGCCAAATGAATGAATGATCAACCCATGTTTAAGCATCATATT 179
 Qy 5032 TATGACCTCTTGTCTGATGATCATTTATGTCATGATGATGATGATGATGATGATGAT 5091
 Db 180 TATGACCTCTTGTCTGATGATCATTTATGTCATGATGATGATGATGATGATGATGAT 239
 Qy 5092 GAAATCTGAGAGACATTTGATTTGCCCATGAAGACCAAGCTTTTCTGCTTGCATAGA 5151
 Db 240 GAAATCTGAGAGACATTTGATTTGCCATGAACACACAGCTTTTCTGCTTGCATAGA 299
 Qy 5152 CTCTCTTGTGGGTGGGGAACAAGAAATCCAGAAGCTGAGAGAGATGAAGAACTCACT 5211
 Db 300 CTCTCTTGTGGGTGGGGAACAAGAAATCCAGAAGCTGAGAGAGATGAAGAACTCACT 359
 Qy 5212 ATTCATATTGGGACTGGCGGAGATGAGAAAAGTGTGACATTTGACAGATGATGATGATG 5271
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Qy 5452 CCTCTTCAGCTGATGATGATATTTGCTGAGTTTACCCCATATGATGTTGTTCCATG 5511
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 Db 659 GATTAAGCTGCCAATTTACGCTTTAGAAATACACTGGAAGAGATTGCTGATCCACTTAC 718
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 Qy 5690 TTGTTG--ACAGTATTTTGAACATGATGCTCCGAAGGACCGTCTTTC 5737
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 VERSION BG575202.1
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 902)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Invitrogen Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: L1AM10574 row: p column: 09
 High quality sequence stop: 869.
 Location/Qualifiers
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 ORIGIN
 Query Match 12.4%; Score 791.8; DB 12; Length 902;
 Best Local Similarity 96.1%; Pred. No. 3.7e-216;
 Matches 833; Conservative 0; Mismatches 32; Indels 2; Gaps 2;
 Db 4497 TGGTGAATTCGCGGAAGATGCTCTGCTGTTTGTATGCTGCTGTGAGTTTCCA 4556
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QY 4557 GACCTCGCTGGCATTTCCTTAGAGCTGTGTCTCTTAAAGAACTGATGGAAGGA 4616
 Db 96 GACCTCGCTGGCATTTCCTTAGAGCTGTGTCTCTTAAAGAACTGATGGAAGGA 155
 QY 4617 ATGCTGCAACCGTGAGCGGGGACAGAGAGCTGTGGCAGCTTCAGAGAGGTTCC 4676
 Db 156 ATGCTGCAACCGTGAGCGGGGACAGAGAGCTGTGGCAGCTTCAGAGAGGTTCC 215
 QY 4677 CTGTCAAGATATCTCTTGTCTCAATGACACATTTGGCCTCAATTTCCCTTCAAGGGT 4736
 Db 216 CTGTCAAGATATCTCTTGTCTCAATGACACATTTGGCCTCAATTTCCCTTCAAGGGT 275
 QY 4737 GGAATGACCGGGAGTCCGTGGCTTCCCTTTTATATAGACCTGCGCAAGTCTGGCAA 4796
 Db 276 GGAATGACCGGGAGTCCGTGGCTTCCCTTTTATATAGACCTGCGCAAGTCTGGCAA 335
 QY 4797 CTTCATGAGATTCACATGAGTGAACCTGACAGTTTGGCTTTGGGGACCAATGACAGCA 4856
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 QY 4857 GAGACGACTCTGTGTGAGAAAGAAACATCTTGAATTTGAGTCCCGCAGAGAGCAAAAT 4916
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 Db 516 GACCTATGGCCAAATGAAAAATGGATCAACACCCATGTTTAAAGACATCAATTTTATGA 575
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 Db 636 CTGAGAGACATTTGATTTTGGCCATGAGACACAGCTTTTCTGCTTGGCATGACTCTT 695
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 Db 696 CTGTGTGCGGTGGGAAACAAGAAATCCAGAGCTGACAGAGATGAAAC-TTCACTATTC 755
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 Db 756 CATATTGGGACTGCGGAGATGACAGAAAGTGTGACATTTGACAGATGATAGAT-GGGA 815
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 VERSION BG576440.1 GI:13584093
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 965)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: DCTD/DP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.383 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 12.3%; Score 787.6; DB 12; Length 965;
 Best Local Similarity 94.1%; Pred. No. 6.3e-215;
 Matches 886; Conservative 0; Mismatches 44; Indels 12; Gaps 6;

QY 5228 GGGGGAGTSCAGAAAAGTGTGACATTTGACAGATGATGATGGAGGTGACAGCCCA 5287
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 QY 5348 GATTGAGAGATGACAAACAGCATGCTTTTATGCAATGGAAGCCCGAGGACCTTTC 5407
 Db 143 GATTGAGAGATGACAAACAGCATGCTTTTATGCAATGGAAGCCCGAGGACCTTTC 202
 QY 5408 GGGGTAAATCTTGAAAACATGACAAATCCAGAACCCCAAGGCTCCCTTTCAGCTGATG 5467
 Db 203 GGGGTAAATCTTGAAAACATGACAAATCCAGAACCCCAAGGCTCCCTTTCAGCTGATG 262
 QY 5468 TAGAATTTTGGCTGAGTTGACCCATATGATCTGTGCTCATGTGATAAGCTGCCAAT 5527
 Db 263 TAGAATTTTGGCTGAGTTGACCCATATGATCTGTGCTCATGTGATAAGCTGCCAAT 322
 QY 5528 TCAGCTTTGAATATACATGAGAGATTTGTGATGCTCACTTTCAGGATGAGGATGCT 5587
 Db 323 TCAGCTTTGAATATACATGAGAGATTTGTGATGCTCACTTTCAGGATGAGGATGCT 382
 QY 5588 CTCAAAGCAGATGACAAATGCTTGCATCATATATGATGAGAAACAATGTCCAGATAC 5647
 Db 383 CTCAAAGCAGATGACAAATGCTTGCATCATATATGATGAGAAACAATGTCCAGATAC 442
 QY 5648 AAGGATCTGCCAAGCATCTCTATCTTCTTTCACAGATGATTTGTGACATATTTTGG 5707
 Db 443 AAGGATCTGCCAAGCATCTCTATCTTCTTTCACAGATGATTTGTGACATATTTTGG 502
 QY 5708 AGCAGTGGCTCGAAGGACCGGCTCTCAAGAAAGTTATGCAAGCAATGACCA 5767
 Db 503 AGCAGTGGCTCGAAGGACCGGCTCTCTCAAGAAAGTTATGCAAGCAATGACCA 562
 QY 5768 TTGACATTAACCGGGAATCTCATGCTTCTTTATATCACTGTATCAGAAATGATGA-T 5826
 Db 563 TTGACATTAACCGGGAATCTCATGCTTCTTTATATCACTGTATCAGAAATGATGA-T 622
 QY 5827 TTCTTTATTTCAATCCAAAGATCTGGGCTATGACTATGCTATCTACAGATTCAGACCA 5886

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Qy	1675	GATCTAGTGAAGATCCCTTTTGATATATCTCATGACCAAAATCCCTTAAAGTGAATTTTC	1734
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Qy	1735	GTTTCACCTGAGCGTCAGACCCCGTAGAAAAGATCAAAAGATCTTCTTGAGATCCCTTTT	1794
Db	674	GTTTCACCTGAGCGTCAGACCCCGTAGAAAAGATCAAAAGATCTTCTTGAGATCCCTTTT	615
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Qy	1855	GCCGGATCAAGAGCTACCAACTCTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT	1914
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Qy	1915	ACCAAAATACCTGTTCTTCTAGTAGACCGGATGAAGGACCACTTCAAGAACTGTAGC	1974
Db	494	ACCAAAATACCTGTTCTTCTAGTAGACCGGATGAAGGACCACTTCAAGAACTGTAGC	435
Qy	1975	ACCGCCTACATTAAGCTGCTCTGCTAATCCTGTTACCAAGTGGCTGCTGCAAGTGGCGATTA	2034
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Qy	2335	GTCATGCTCGTCAAGGGGGCGAGCCCTTATGAAAAACGACAGCAACCGGCGCTTTTAAACG	2394
Db	74	GTCATGCTCGTCAAGGGGGCGAGCCCTTATGAAAAACGACAGCAACCGGCGCTTTTAAACG	15
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Db	14	GTTCTCTGGCTTTT 1	
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AJ281449/c			
LOCUS			
DEFINITION			
4A3A-P4D5-F Anopheles gambiae immune competent 4A3A Anopheles			
gambiae cDNA clone 4A3A-P4D5, mRNA sequence.			
ACCESSION			
AJ281449			
VERSION			
AJ281449.1 GI:6929329			
KEYWORDS			
EST.			
SOURCE			
ORGANISM			
Anopheles gambiae (African malaria mosquito)			
Anopheles gambiae			
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
Neoptera; Endopterygota; Diptera; Nematocera; Culicoides;			
Anopheles.			
1 (bases 1 to 800)			
REFERENCE			
Dimopoulos,G., Castejant,T.L., Chang,S., Scheetz,T., Roberts,C.,			

Donohue, M., Schultz, J., Benes, V., Bork, P., Ansoerge, W., Soares, M.B., and Kafatos, F.C.
 Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
 Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)

JOURNAL MEDLINE PUBLISHED 20300950 10841561

COMMENT Contact: Dimopoulos G
 Fotis C. Kafatos Laboratory
 European Molecular Biology Laboratory
 Meyerhofstrasse 1, 69117 Heidelberg, Germany.
 Location/Qualifiers
 1. 800
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
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 /db_xref="taxon:7165"
 /clone="4A3A-P4D5"
 /cell_line="immune competent 4A3A"
 /lab_host="E. coli DH10B"
 /clone_lib="Anopheles gambiae immune competent 4A3A"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Bonaldi, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches to Facilitate Gene Discovery, Genome Research 6, 791-806."

ORIGIN

Query Match 12.2%; Score 779.4; DB 9; Length 800;
 Best Local Similarity 99.2%; Pred. No. 1,3e-212;
 Matches 783; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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 800 ACTTATGATGATTAAACCTTCAATTTTAAATTAAGAGATAGAGTGAAGATCCTTTT 741

Qy 1696 TGTATATTCATGACCAAAATCCCTTAACGTGAGTTTCTTCCATCGAGCGTCAAGACC 1755
 740 TGTATATTCATGACCAAAATCCCTTAACGTGAGTTTCTTCCATCGAGCGTCAAGACC 681

Db 1756 CGTAAAGAAAGATCAAGAGATCTTCTTGAGATCCTTTTCTGCGCGTAACTGTCGCT 1815
 680 CGTAAAGAAAGATCAAGAGATCTTCTTGAGATCCTTTTCTGCGCGTAACTGTCGCT 621

Qy 1816 GCAAAACAAAAAACAACCGCTACAGCGGTGTTTGTTCGCGATCAAGAGCTACCAAC 1875
 620 GCAAAACAAAAAACAACCGCTACAGCGGTGTTTGTTCGCGATCAAGAGCTACCAAC 561

Db 1876 TCTTTTTCGAGAGTAAGTGGCTTCAGCAGAGCGGAGATCAAAATACGTTCTTCTAGT 1935
 560 TCTTTTTCGAGAGTAAGTGGCTTCAGCAGAGCGGAGATCAAAATACGTTCTTCTAGT 501

Qy 1936 GTAGCGGTAGTTAGGCGACCACTTCAAGAACTGTGAGACCGGCTTACATACCTCGCT 1995
 500 GTAGCGGTAGTTAGGCGCGACCACTTCAAGAACTGTGAGACCGGCTTACATACCTCGCT 441

Db 1996 GCTAATCTGTTTACGATGAGCTGCTGCGAGTGGCGATGATGCTGTTTACCGAGTTGA 2055
 440 GCTAATCTGTTTACGATGAGCTGCTGCGAGTGGCGATGATGCTGTTTACCGAGTTGA 381

Qy 2056 CTGAAGACATAGTTACCGGATTAAGCGGCGCGGTGCGGCTGAACGGGGGCTTCGTCAC 2115
 380 CTGAAGACATAGTTACCGGATTAAGCGGCGCGGTGCGGCTGAACGGGGGCTTCGTCAC 321

Db 2116 ACAGCCAGCTTGAGAGGAAGCACTTACACGGAAGTGAATACCTACAGCGTGAAGTATG 2175
 320 ACAGCCAGCTTGAGAGGAAGCACTTACACGGAAGTGAATACCTACAGCGTGAAGTATG 261

Qy 2176 AGAAGGCGCACCGCTTCCGAAAGGAGAAAGGCGGACAGGTATCCGTTAAACGGCAAGGT 2235

Db 260 AGAAGCGCGACAGCTTCCGGAAGGAGAAAGCGGACAGGTATCCGTTAAGCGGAGGCT 201

Qy 2236 CGAAGAGAGAGCGGACAGAGGAGGAGCTTCCAGGGGGAAACGCTGTATCTTATATAGCC 2295
 200 CGAAGAGAGAGCGGACAGAGGAGGAGCTTCCAGGGGGAAACGCTGTATCTTATATAGCC 141

Qy 2296 TGTGCGGTTTCCGACACCTTCTGACTGAGCGTGCATTTTGTGATGCTCTCAAGGGGGCG 2355
 140 TGTGCGGTTTCCGACACCTTCTGACTGAGCGTGCATTTTGTGATGCTCTCAAGGGGGCG 81

Db 2356 GAGCTTATGAAAACGCGACGAGAGCGGCGCTTTTACGTTTCTGAGCTTTTCTGCGCC 2415
 80 GAGCTTATGAAAACGCGACGAGAGCGGCGCTTTTACGTTTCTGAGCTTTTCTGCGCC 21

Qy 2416 TTTTGCTCA 2424

Db 20 GCAAGCTTA 12

RESULT 14
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 5', mRNA sequence.
 ACCESSION BUI79860
 VERSION BUI79860.1 GI:22693844
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 939)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: DCTD/DRP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN

Query Match 12.1%; Score 772.2; DB 13; Length 939;
 Best Local Similarity 93.0%; Pred. No. 1.7e-210;
 Matches 863; Conservative 0; Mismatches 56; Indels 9; Gaps 5;

Db 5446 AGGCTCCCTCTTCACTATGATGAAATTTTGCTGAGTGAACCAATATGATTCGT 5505
 1 AGGCTCCCTCTTCACTATGATGAAATTTTGCTGAGTGAACCAATATGATTCGT 60


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Db      488 ATGAAAAATGATCAACACCCATGTTTAAAGACATCATATTTATGACCTTTTGTG 547
QY      5050 ATGCATTATTATGTGTCAATGATGACATGCTTGGGGATATGAAATCTGAGACATT 5109
Db      548 ATGCATTATTATGTGTCAATGATGACATGCTTGGGGATCTGAAATCTGAGACATT 607
QY      5110 GATTTTGCCCATGAGCACCAGCTTTTCTGCTTGGCATAGACTCTTCTTGTTCGGTGG 5169
Db      608 GATTTTGCCCATGAGCACCAGCTTTTCTGCTTGGCATAGACTCTTCTTGTTCGGTGG 667
QY      5170 GAACAAAGAAATCCAGAGCTGACAGAGATGAAAACTTCACTATTTCATATTGGACTGG 5229
Db      668 GAACAAAGAAATCCAGAGCTGACAGAGATGAAAACTTCACTATTTCATATTGGACTGG 727
QY      5230 CGGGATGCAAGAAAGTGTGCAATTGTGACAGATGA--GTACATGGAGAGTCAACCCCA 5287
Db      728 CGGGATGCAAGAAAGTGTGCAATTGTGACAGATGAAGTACTTGGAGGGGTCAACCA 787
QY      5288 CAAATCCTAATT 5300
Db      788 CAAATCCTAATT 800
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